

Access DB# 76027

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
 Reference Librarian
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Searcher: Jan
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Type of Search

NA Sequence (#) _____
 AA Sequence (#) ☒ _____
 Structure (#) _____
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 Patent Family _____
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 Other (specify) _____

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:12:57 ; Search time 75.12 Seconds
(without alignments)
294.245 Million cell updates/sec

Title: US-09-383-551B-2

Perfect score: 1082

Sequence: 1 MKSLGWFFELCLRIKVLGTG.....YMFMRVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

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4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
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21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1082	100.0	199	AAW75956	Human cell surface
2	1082	100.0	199	AAW75957	Human cell surface
3	1082	100.0	199	AAW08026	Human activated T-
4	1082	100.0	199	AAW08731	Amino acid sequenc
5	1082	100.0	199	AAW03428	Human gene 2 encod
6	1082	100.0	199	AAE03460	Human gene 2 encod
7	1082	100.0	199	AAE03525	Human secreted pro
8	1066.5	98.6	198	AAW92213	Human Th2-specific
9	737.5	68.2	200	AAW92212	Murine Th2-specific
10	734	67.8	200	AAW08723	Amino acid sequenc
11	722.5	66.8	200	AAW75958	Mouse cell surface

12	701	64.8	200	19	AAW71874	Rat cell surface p
13	696	64.3	216	19	AAW71875	Rat cell surface p
14	658	60.8	379	22	AAW67716	Amino acid sequenc
15	449.5	41.5	380	22	AAW67717	Amino acid sequenc
16	146.5	13.5	225	20	AAW41136	Rat CD28 protein s
17	145.5	13.4	221	21	AAW32286	Feline CD28. Feli
18	145.5	13.4	221	21	AAW32279	Cat CD28 receptor.
19	139.5	12.9	220	13	AAW20805	Human CD28 antigen
20	139.5	12.9	220	13	AAW27103	Sequence encoded b
21	139.5	12.9	220	17	AAW02131	Human CD28 CDNA pr
22	139.5	12.9	220	17	AAW91433	Human CD28 antigen
23	139.5	12.9	220	18	AAW38413	CD28. Homo sapien
24	139.5	12.9	220	19	AAW80442	Human CD28 antigen
25	139.5	12.9	220	20	AAW88451	Human CD28 antigen
26	139.5	12.9	220	21	AAW96128	Human cell surface
27	139.5	12.9	220	21	AAW44294	Human CD28 recepto
28	139.5	12.9	220	22	AAU02437	Human lymphocyte c
29	134	12.4	225	20	AAW41135	Mouse CD28 protein
30	126	11.6	223	20	AAW41137	Human CD28 protein
31	120.5	11.1	367	18	AAW35862	Human CD28:IgG2a c
32	119.5	11.0	134	18	AAW35846	Human CD28 for use
33	119.5	11.0	152	16	AAW67706	CD28 extracellular
34	89.5	8.3	117	20	AAW24469	Human CD28 gene pr
35	89	8.2	305	22	AAW66371	Human partial olfa
36	89	8.2	319	22	AAW71916	Human olfactory re
37	89	8.2	321	22	AAW46999	Human OLFXY protei
38	87.5	8.1	213	22	AAE04561	Human G-protein co
39	87	8.0	330	8	AAW70445	Sequence of mouse
40	86	7.9	223	18	AAW25111	Soluble human CTLA
41	86	7.9	223	22	AAW66519	Human CTLA4. Homo
42	86	7.9	223	22	AAU00687	Human CTLA4 protei
43	85.5	7.9	187	19	AAW29728	Soluble CTLA4 muta
44	84.5	7.8	209	21	AAW94998	Human secreted pro
45	84	7.8	223	21	AAW15129	Human CTLA-4 prote

ALIGNMENTS

RESULT 1

AAW75956

ID AAW75956 standard; Protein; 199 AA.

XX

AC AAW75956;

XX

DT 11-DEC-1998 (first entry)

XX

DE Human cell surface protein #1.

XX

KW Human; cell surface protein; thymocyte; lymphocyte; cell adhesion; signal transmission; autoimmune disorder; allergy; diagnosis;

KW mitogen-stimulated.

XX

OS Homo sapiens.

XX

PN WO9838216-A1.

XX

PD 03-SEP-1998.

XX

PF 27-FEB-1998; 98WO-JP00837.

XX

PR 26-FEB-1998; 98JP-0062217.

XX

PR 27-FEB-1997; 97JP-0062290.

XX

PA (NISR) JAPAN TOBACCO INC.

XX

PI Tamatani T, Tezuka K;

XX

WPI; 1998-481144/41.

DR N-PSDB; AAW53198.

XX

PT Cell surface molecule expressed in thymocytes and lymphocytes and mediating signal transmission and cell adhesion, and antibodies to

PT it useful in treatment of auto:immune and allergic disorders.

XX
PS Claim 2; Page 99-101; 149pp; Japanese.

XX
CC The present sequence represents a human cell surface protein which is expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell surface protein induces adhesion of mitogen-stimulated lymphocytes to antibodies recognising the cell surface protein. These antibodies also produce an increase in peripheral blood lymphocytes in the presence of an antibody recognising CD3 antigen. The cell surface protein contains the amino acid sequence FDPFPF in its extracellular region and the sequence YMF in its intracellular region. The cell surface protein can be used in the prevention and treatment of autoimmune and allergic diseases, and in the diagnosis and investigation of such disorders.

XX Sequence 199 AA;

Query Match 100.0%; Score 1082; DB 19; Length 199;
Best Local Similarity 100.0%; Pred. No. 6.6e-116;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKSGLWYFFLCRLIKVLTEINGSANYEMFIFHNGGVQVILCKYDPDIVQOFKMQLLKGQ 60

Db 1 mksglwyfflclrlkvltgeingsanyemfifhnggvqilckypdivqfkmqlkggq 60

QY 61 ILCDLTKTGSGNTVSIKSLKFSCHSOLSNNSVSFFLYNLDSHANYFCNLSTFDPPPPK 120

Db 61 ilcdltktgsgntvsikskslkschsqslsnnsvsfflynldshanyfncnlstfppppk 120

QY 121 VLTGGYLHIYESQLCCQLKFWLPICGAAVVFVVCILGCLICWLTKKKYSSSVHPNGEY 180

Db 121 vltggylhiyesqlccqlkfwlpigcaafvvvcilgcllcwltkkysssvhpdngey 180

QY 181 MFMRAVNTAKKSLRLTDVTL 199

Db 181 mfmravntakkarltdvtl 199

RESULT 2

AAW75957

ID AAW75957 standard; Protein; 199 AA.

AC AAW75957;

DT 11-DEC-1998 (first entry)

DE Human cell surface protein #2.

Human; cell surface protein; thymocyte; lymphocyte; cell adhesion; signal transmission; autoimmune disorder; allergy; diagnosis; mitogen-stimulated.

KW Homo sapiens.

OS WO9838216-A1.

PN 03-SEP-1998.

PD 27-FEB-1998; 98WO-JP00837.

XX 26-FEB-1998; 98JP-0062217.

XX 27-FEB-1997; 97JP-0062290.

PA (NISR) JAPAN TOBACCO INC.

XX Tamatani T, Tezuka K;

PI WPI; 1998-481144/41.

XX N-PSDB; AAV53199.

PT Cell surface molecule expressed in thymocytes and lymphocytes and -

PT mediating signal transmission and cell adhesion, and antibodies to

PT it useful in treatment of auto:immune and allergic disorders.

XX
PS Claim 9; Page 101-105; 149pp; Japanese.

XX
CC The present sequence represents a human cell surface protein which is expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell surface protein induces adhesion of mitogen-stimulated lymphocytes to antibodies recognising the cell surface protein. These antibodies also produce an increase in peripheral blood lymphocytes in the presence of an antibody recognising CD3 antigen. The cell surface protein contains the amino acid sequence FDPFPF in its extracellular region and the sequence YMF in its intracellular region. The cell surface protein can be used in the prevention and treatment of autoimmune and allergic diseases, and in the diagnosis and investigation of such disorders.

XX Sequence 199 AA;

Query Match 100.0%; Score 1082; DB 19; Length 199;
Best Local Similarity 100.0%; Pred. No. 6.6e-116;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSGLWYFFLCRLIKVLTEINGSANYEMFIFHNGGVQVILCKYDPDIVQOFKMQLLKGQ 60

Db 1 mksglwyfflclrlkvltgeingsanyemfifhnggvqilckypdivqfkmqlkggq 60

QY 61 ILCDLTKTGSGNTVSIKSLKFSCHSOLSNNSVSFFLYNLDSHANYFCNLSTFDPPPPK 120

Db 61 ilcdltktgsgntvsikskslkschsqslsnnsvsfflynldshanyfncnlstfppppk 120

QY 121 VLTGGYLHIYESQLCCQLKFWLPICGAAVVFVVCILGCLICWLTKKKYSSSVHPNGEY 180

Db 121 vltggylhiyesqlccqlkfwlpigcaafvvvcilgcllcwltkkysssvhpdngey 180

QY 181 MFMRAVNTAKKSLRLTDVTL 199

Db 181 mfmravntakkarltdvtl 199

RESULT 3

AAW08026

ID AAW08026 standard; Protein; 199 AA.

AC AAW08026;

DT 08-JUL-1999 (first entry)

DE Human activated T-lymphocyte protein 8F4.

T-lymphocyte; human; 8F4; T cell co-stimulation; activated; CD4+; CD8+; anticancer; antiviral; anti-asthma; immunomodulator; proliferation; T cell activation; cytokine synthesis; regulatory element; B cell; T cell-dependent antibody production; treatment; prevention; cancer; autoimmune disease; transplant rejection; immune system regulation; disorder; acquired immune deficiency syndrome; AIDS; asthma.

OS Homo sapiens.

PN WO9915553-A2.

XX 01-APR-1999.

XX 23-SEP-1998; 98WO-DE02896.

XX 11-MAY-1998; 98DE-1021060.

XX 23-SEP-1997; 97DE-1041929.

PA (DEKO-) DEUT KOCH INST ROBERT.

PA (BUND) BUNDESREPUBLIK DEUT PAUL-EHRlich-INST.

XX Krocsek R;

XX WPI; 1999-276975/23.

DR N-PSDB; AAX37661.
 XX Polypeptide 8F4 co-stimulates T cells and is present only on
 PT activated cells
 XX
 XX Claim 2; Page 24; 47pp; German.
 XX This invention describes a novel human protein, 8F4, and its encoding
 CC nucleic acid which co-stimulates T cells and is present on activated CD4+
 CC and CD8+ T cells but not on resting or activated B cells, granulocytes,
 CC monocytes, natural killer or dendritic cells. 8F4 has anticancer,
 CC antiviral, anti-asthma and immunomodulatory activity. 8F4 provides a
 CC strong co-stimulatory signal for T cell activation, i.e. it amplifies
 CC proliferation of T cells, synthesis of certain cytokines and other
 CC regulatory agents, and improves T cell-dependent antibody production
 CC by B cells. Agents that inhibit 8F4 are used to treat or prevent
 CC autoimmune diseases, to prevent transplant rejection and to treat
 CC disorders of immune system regulation. 8F4, or cells that express it,
 CC is/are used to treat or prevent cancers, acquired immune deficiency
 CC syndrome, asthma and chronic infectious diseases (e.g. hepatitis B or C).
 XX
 XX Sequence 199 AA;
 PS Disclosure; Fig 13A; 174pp; English.
 XX
 CC The present sequence represents a CRP1 (CD28 related protein-1)
 CC polypeptide. The specification also describes a B7RP1 (B7 related
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
 CC predicted to be a type I transmembrane protein. The nucleic acids are
 CC useful for regulating T cell activation or proliferation in an animal.
 CC The polypeptides are useful for treating, preventing ameliorating or
 CC diagnosing a T-cell mediated disorder in an animal. They can also be
 CC used to identify test molecules that bind to the polypeptides.
 XX
 XX Sequence 199 AA;
 PS
 CC
 CC Query Match 100.0%; Score 1082; DB 20; Length 199;
 CC Best Local Similarity 100.0%; Pred. No. 6.6e-116;
 CC Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKSGLWYFFLCRLIKVLTGEINGSANYEMFIHNGGVQILCKYPDIVQOQFMQLLKGGQ 60
 DB 1 mksglwyfflclrlkvlkteingsanyemfihnggvqilckypdivqgfmqlkkggq 60
 QY 61 ILCDLTKTGSGNTVSIKSLKFCCHSOLSNNVSFFLYNLDSHANYFCNLSIFDPPPPK 120
 DB 61 ilcdltktgsgntvsiksikfchsqslsnsvsfflynldshanyfncnlsifdppppk 120
 QY 121 VTLTGGYHLHYESQLCCQLKFWLPICGAFFVYVVCILGCLICWLTKKKYSSSVHPDNGEY 180
 DB 121 vlttggylhiesqlccqlkfwlpigcaafvvyvvcilgclilcwltkkkysssvhpdngey 180
 QY 181 MFMRVNTAKKSRLTDVTL 199
 DB 181 mfmravntakksrltdvtl 199
 RESULT 4
 AAB08731
 AAB08731 standard; Protein; 199 AA.
 AAB08731;
 XX
 DT 02-JAN-2001 (first entry)
 XX Amino acid sequence of a human CRP1 polypeptide.
 DE CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;
 KW T-lymphocyte activation; type I transmembrane protein; T cell activation;
 KW T cell proliferation; T-cell mediated disorder.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..20
 FT /note= "signal peptide"
 FT Protein 21..199
 FT /note= "mature protein"
 FT Domain 21..140
 FT /note= "extracellular domain"
 FT Domain 141..161
 FT /note= "predicted transmembrane domain"
 FT Domain 162..199
 FT /note= "intracellular domain"
 XX

PN WO200046240-A2.
 XX
 PD 10-AUG-2000.
 XX
 XX 27-JAN-2000; 2000WO-US01871.
 XX
 XX 03-FEB-1999; 99US-0244448.
 PR 08-MAR-1999; 99US-0264527.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Yoshinaga SK;
 PI
 XX WPI; 2000-543476/49.
 DR N-PSDB; AAA64558.
 XX
 XX Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
 PT in the treatment, prevention and diagnosis of T cell mediated disorders
 PT
 XX
 PS Disclosure; Fig 13A; 174pp; English.
 XX
 CC The present sequence represents a CRP1 (CD28 related protein-1)
 CC polypeptide. The specification also describes a B7RP1 (B7 related
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
 CC predicted to be a type I transmembrane protein. The nucleic acids are
 CC useful for regulating T cell activation or proliferation in an animal.
 CC The polypeptides are useful for treating, preventing ameliorating or
 CC diagnosing a T-cell mediated disorder in an animal. They can also be
 CC used to identify test molecules that bind to the polypeptides.
 XX
 XX Sequence 199 AA;
 PS
 CC
 CC Query Match 100.0%; Score 1082; DB 21; Length 199;
 CC Best Local Similarity 100.0%; Pred. No. 6.6e-116;
 CC Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 mksglwyfflclrlkvlkteingsanyemfihnggvqilckypdivqgfmqlkkggq 60
 QY 61 ILCDLTKTGSGNTVSIKSLKFCCHSOLSNNVSFFLYNLDSHANYFCNLSIFDPPPPK 120
 DB 61 ilcdltktgsgntvsiksikfchsqslsnsvsfflynldshanyfncnlsifdppppk 120
 QY 121 VTLTGGYHLHYESQLCCQLKFWLPICGAFFVYVVCILGCLICWLTKKKYSSSVHPDNGEY 180
 DB 121 vlttggylhiesqlccqlkfwlpigcaafvvyvvcilgclilcwltkkkysssvhpdngey 180
 QY 181 MFMRVNTAKKSRLTDVTL 199
 DB 181 mfmravntakksrltdvtl 199
 RESULT 5
 AAE03428
 ID AAE03428 standard; Protein; 199 AA.
 XX
 XX AAE03428;
 XX
 DT 10-AUG-2001 (first entry)
 XX Human gene 2 encoded secreted protein H72SG64, SEQ ID NO: 111.
 DE
 XX Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disease; AIDS; autoimmune disease; rheumatoid arthritis;
 KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
 KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
 KW inflammation; neurological disorder; Alzheimer's disease; food additive;
 KW angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;
 KW

the new genes. Specific uses are described for each of the 32 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, anglogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.

Sequence 199 AA;

Query Match 100.0%; Score 1082; DB 22; Length 199;
Best Local Similarity 100.0%; Pred. No. 6.6e-116; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0;

QY 1 MKSGLWYFFLCIRIKVLTGEINGSANYEMFIHNGGVQILCKYDIPVQOQFMQLKGQ 60
Db 1 mksglwyfflclrikvltgeingsanyemfifhnggvqilckypdivqfkmqlkgq 60

QY 61 ILCDLTKTGSGNTVSIKSLKFCCHSOLNSNSVSFFLYNLDSHANYFCNLISFPPPPK 120
Db 61 ilcdltktgsgntvsiikslkfcchsglslnsnsvsfflynlshanyfncnlisfppppk 120

QY 121 VLTGGYLIHYESQCCOLKFWLPICGAFFVVCVILGCLICWLTKKKYSSSVHPDNGEY 180
Db 121 vltggylihyesqccqlkfwlpigcaafvvcvllgcllclwltkkylsssvhpdngey 180

QY 181 MPMRAVNTAKSRRLTDVTL 199
Db 181 mpmravntaksrldvtl 199

RESULT 7

AAE03525 standard; Protein; 199 AA.

AC AAE03525;

XX

XX 10-AUG-2001 (first entry)

XX Human secreted protein variant, SEQ ID NO: 211.

DE

XX Human: secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; anglogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnery; binding partner identification; gene therapy.

OS Homo sapiens.

XX WO200132675-A1.

PN

XX 10-MAY-2001.

PD

XX 25-OCT-2000; 2000WO-US29363.

XX

XX 29-OCT-1999; 99US-0162239.

PR 30-JUN-2000; 2000US-0215139.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

XX

PI Ruben SM, Komatsoulis GA, Wei P, Baker KP, Young PE;

XX WPI; 2001-328772/34.

DR

XX Thirty two human secreted proteins, useful for treating cancers, hyperproliferative disorders, inflammatory disorders, neurological disorders, autoimmune diseases and cardiovascular disorders.

PT

PT Disclosure; Page 524; 576pp; English.

PS

XX AAD07809-AAD07907 represent cDNAs corresponding to 32 human secreted protein genes, and AAE03427-AAE03523 represent the proteins they encode. AAE03524-AAE03537 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. CC pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 32 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, anglogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein variant of the invention.

XX

SQ Sequence 199 AA;

Query Match 100.0%; Score 1082; DB 22; Length 199;
Best Local Similarity 100.0%; Pred. No. 6.6e-116; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0;

QY 1 MKSGLWYFFLCIRIKVLTGEINGSANYEMFIHNGGVQILCKYDIPVQOQFMQLKGQ 60
Db 1 mksglwyfflclrikvltgeingsanyemfifhnggvqilckypdivqfkmqlkgq 60

QY 61 ILCDLTKTGSGNTVSIKSLKFCCHSOLNSNSVSFFLYNLDSHANYFCNLISFPPPPK 120
Db 61 ilcdltktgsgntvsiikslkfcchsglslnsnsvsfflynlshanyfncnlisfppppk 120

QY 121 VLTGGYLIHYESQCCOLKFWLPICGAFFVVCVILGCLICWLTKKKYSSSVHPDNGEY 180
Db 121 vltggylihyesqccqlkfwlpigcaafvvcvllgcllclwltkkylsssvhpdngey 180

QY 181 MPMRAVNTAKSRRLTDVTL 199
Db 181 mpmravntaksrldvtl 199

AA92213	1	mksglwyfflclrikvltgelngsanyemfihngvgqilckypdivqfkmqlkggq	60
XX			
AC	61	ILCDLTKTKSGNVTSTKSLKCHSOLSNNSVSFFLYNLDSHANYFCNLSIFDPPPK	120
XX			
DT	61	ilcdltkktgsgntvsklskchsqslsnnsvsfflynldhshanyfncnlsifdppfk	120
XX			
DE	121	VTUTGVLHYESQCLQCFWLPICGAAPVVCILGCLICILWLTKKYSKSSSVHDPNGEY	180
XX			
KW	121	vtitggyllhiesqclqcfwlpigcaafvvcvllgcllicwlt-kkysssvhdpngey	179
KW			
KW	181	MFMRVNTAKKSRSLTDVTL	199
XX			
OS	180	mfmrvntakksrldvtl	198
XX			
FT	Key	Location/Qualifiers	
FT	Peptide	113..118	
FT		/label= conserved_PPP_motif	
		/note= "common in CD28 and CTLA-4"	
	Peptide	178..181	
		/label= YXXM_motif	
		/note= "common in CD28 and CTLA-4; necessary for CD28-mediated phosphatidylinositol 3-kinase activity"	
PN	WO200019988-A1.		
XX	13-APR-2000.		
XX	06-OCT-1999;	99WO-US23156.	
XX	07-OCT-1998;	98US-0168229.	
PR	26-FEB-1999;	99US-0258670.	
PR	06-OCT-1999;	99US-0413136.	
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX	Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J;		
XX	WPI; 2000-303619/26.		
DR	N-PSDB; AAA09056.		
XX			
PT	T helper (Th) 2 nucleic acids and encoded proteins, useful for the diagnosis and treatment of immune and respiratory disorders such as Crohn's diseases, arthritis, insulin dependent diabetes and autoimmunity		
XX			
XX	Claim 16; Page 138-139; 159pp; English.		
CC	This Th2-specific polypeptide, which has similarity to human CD28 and human CTLA-4 is encoded by human orthologue h1228.		
CC	A novel method for modulating a Th2 response, an immune response, or suppressing airway inflammation or hyperresponsiveness in a mammal comprises administering a Th2-specific polypeptide of the invention, an antibody to such a polypeptide or allelic variants of the genes. The novel DNA and polypeptide sequences are useful for treatment and diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases, arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis, dermatitis, psoriasis, graft rejection, graft versus host diseases, sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis, viral infections (including human immunodeficiency virus (HIV)), bacterial infections, bronchitis, cystic fibrosis, diphtheria, emphysema, pneumonia, and Legionnaires disease.		
XX			
SQ	Sequence	198 AA;	
	Query Match	98.6%;	Score 1066.5; DB 21; Length 198;
	Best Local Similarity	99.5%;	Pred. No. 3.9e-114;
	Matches 198; Conservative	0; Mismatches 0; Indels 1; Gaps 1;	
QY	1	MKSGLWYFFLCLRIKVLTEINGSANYEMFIFHNGVGQILCKYPDIVQFQKMLKGGQ	60

DR	WPI; 1998-481144/41.	DR	WPI; 1998-481144/41.
XX	N-PSDB; AAV61358.	XX	N-PSDB; AAF79939.
XX		XX	
PT	Cell surface molecule expressed in thymocytes and lymphocytes to	PT	New isolated nucleic acid encoding a GL50 polypeptide for modulating a
PT	mediating signal transmission and cell adhesion, and antibodies to	PT	immune response and reducing the proliferation of a tumour cell.
XX	it useful in treatment of auto-immune and allergic disorders.	XX	
PS	Claim 9; Page 112-115; 149pp; Japanese.	PS	Disclosure; Fig 26B; 195pp; English.
XX		XX	
CC	The present sequence represents a rat cell surface protein which is	CC	The present sequence represents a fusion protein, comprising human ICOS
CC	expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell	CC	(hICOS) and murine IgG2a (mIGG2A). The fusion protein is used in the
CC	surface protein induces adhesion of mitogen-stimulated lymphocytes to	CC	course of the invention. The specification describes GL50 polypeptides.
CC	antibodies recognising the cell surface protein. These antibodies also	CC	GL50 molecules are antigens on the surface of antigen presenting cells,
CC	produce an increase in peripheral blood lymphocytes in the presence of	CC	which costimulate T cell proliferation and bind to costimulatory receptor
CC	an antibody recognising CD3 antigen. The cell surface protein contains	CC	ligands on T cells. GL50 modulating agents are used to modulate an immune
CC	the amino acid sequence FDPDPF in its extracellular region and the	CC	response in a subject. GL50 polypeptides are used to modulate T cell
CC	sequence YVFM in its intracellular region. The cell surface protein can	CC	costimulation, and to reduce the proliferation of a tumour cell. Diseases
CC	be used in the prevention and treatment of autoimmune and allergic	CC	that can be treated using GL50 molecules are graft-versus-host disease,
CC	diseases, and in the diagnosis and investigation of such disorders.	CC	autoimmune disease, allergies, acquired immune deficiency syndrome
XX		CC	(AIDS), and viral infections. The GL50 molecules can be used in vaccines.
XX	Sequence 216 AA;	CC	GL50 polynucleotides can be used to locate gene regions associated with
XX		CC	genetic disease, in tissue typing, and in forensic identification of a
XX		CC	biological sample.
XX		XX	Sequence 379 AA;
XX		XX	
XX	Query Match 64.3%; Score 696; DB 19; Length 216;	XX	Query Match 60.8%; Score 658; DB 22; Length 379;
XX	Best Local Similarity 68.8%; Pred. No. 1.5e-71;	XX	Best Local Similarity 100.0%; Pred. No. 7.4e-67;
XX	Matches 132; Conservative 16; Mismatches 40; Indels 4; Gaps 2;	XX	Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	7 YF---FLFCLIRIKVLTEINGSNANYEMFIHNGVGQILCKYDPDIVQOFKMQLLKGGQILIC 63	QY	21 EINGSANYEMFIHNGVGQILCKYDPDIVQOFKMQLLKGGQILCKYDKSGNVTVSIXSL 80
DB	4 Yfscvfvfclllkllgeindlanhrmfshdgvgqiscnypetvqqlkmqlfkrevlc 63	DB	26 eingsanyemfifhngvgqilckypdivqgfkmgqllkggqilcdltkkgsgntvsixsl 85
QY	64 DLTKTKGSGNTVSIKSLKFKCHSOLSNNSVSFFLYNLHDHSHANYFCNLSIFDPPPF-KVT 122	QY	81 KFKCHSOLSNNSVSFFLYNLHDHSHANYFCNLSIFDPPPFKVTLTGGYLHIYESOLCCOLK 140
DB	64 dlktksgntvsiknpsqylsnnsvsffldnadssggsyflcslsifdpppfqekn 123	DB	86 kfchsqslsnnsvsfflynlhdshanyfncnlisfidpppfkvtltggylhiyesqlcqlk 145
QY	123 LTGGYLHIYESOLCCOLKFWLPITGCAAFVVCILGILICLWLTKKKYSVSDHPNCEYMF 182	QY	141 F 141
DB	124 lsggyliyesqlccqclklwlpvgcaafvaallfgcifiwfvakkkyrsvhdnpnseymf 183	DB	146 f 146
QY	183 MRAVNTAKKSLR 194	XX	RESULT 15
DB	184 maavntakksrl 195	XX	AAB67716
XX		XX	ID AAB67716 standard; Protein; 379 AA.
XX		XX	AAB67716;
XX	11-JUN-2001 (first entry)	XX	11-JUN-2001 (first entry)
XX	Amino acid sequence of hICOS-mIgG2am fusion protein.	XX	Amino acid sequence of mICOS-mIgG2am fusion protein.
XX	GL50; antigen; antigen presenting cell; T cell proliferation; tumour;	XX	GL50; antigen; antigen presenting cell; T cell proliferation; tumour;
KW	graft-versus-host disease; autoimmune disease; allergy; viral infection;	KW	graft-versus-host disease; autoimmune disease; allergy; viral infection;
KW	acquired immune deficiency syndrome; AIDS; vaccine.	KW	acquired immune deficiency syndrome; AIDS; vaccine.
OS	Synthetic.	OS	Synthetic.
OS	Homo sapiens.	OS	Mus musculus.
XX	Mus musculus.	XX	WO200121796-A2.
XX	WO200121796-A2.	XX	29-MAR-2001.
XX	21-SEP-2000; 2000WO-US25892.	XX	21-SEP-2000; 2000WO-US25892.
XX	21-SEP-1999; 99US-0155043.	XX	21-SEP-1999; 99US-0155043.
XX	(GEMY) GENETICS INST INC.	XX	(GEMY) GENETICS INST INC.
XX	Ling V, Dunussi-Joannopolulos K;	XX	Ling V, Dunussi-Joannopolulos K;

DR WPI; 2001-244938/25.
DR N-PSDB; AAF79940.
XX
PT New isolated nucleic acid encoding a GL50 polypeptide for modulating a
PT immune response and reducing the proliferation of a tumour cell -
XX
PS Disclosure; Fig 27B; 195pp; English.
XX
CC The present sequence represents a fusion protein, comprising murine ICOS
CC (mICOS) and murine IgG2a (mIgG2A). The fusion protein is used in the
CC course of the invention. The specification describes GL50 polypeptides.
CC GL50 molecules are antigens on the surface of antigen presenting cells,
CC which costimulate T cell proliferation and bind to costimulatory receptor
CC ligands on T cells. GL50 modulating agents are used to modulate an immune
CC response in a subject. GL50 polypeptides are used to modulate T cell
CC costimulation, and to reduce the proliferation of a tumour cell. Diseases
CC that can be treated using GL50 molecules are graft-versus-host disease,
CC autoimmune disease, allergies, acquired immune deficiency syndrome
CC (AIDS), and viral infections. The GL50 molecules can be used in vaccines.
CC GL50 polynucleotides can be used to locate gene regions associated with
CC genetic disease, in tissue typing, and in forensic identification of a
CC biological sample.
XX
SQ Sequence 380 AA;

Query Match 41.5%; Score 449.5; DB 22; Length 380;
Best Local Similarity 70.2%; Pred. No. 6.5e-43;
Matches 85; Conservative 13; Mismatches 22; Indels 1; Gaps 1;
QY 21 EINGSANYEMFIHNGGVOILCKYDPDVOQFRMQLKGGQILCDLTKTKSGNTVSIKSL 80
Db : |||||: || ||||| |||||: || |||||: |||||: |||||: |||||: |||||:
26 eingsadhrmfsfhnggvqiskypetvqqlkmrlfrerevliceltktkgsgnavsiknp 85
QY 81 KECHSOLSNNSVSEFLYNLDHSHANYFCNLSIFDPPPKV-TLTGGYLHIYESQLCCOL 139
Db : ||||| || || ||||| || || ||||| |||||: ||||| ||||| ||||| |||||
86 mlclyhlnsnsvsfflnnpdsqggyfcslsifdpppfqernlsqgyihyiesqlccoql 145
QY 140: K 140
Db : |
146 k 146

Search completed: September 18, 2002, 15:26:25
Job time: 808 sec

GenCore version 4.5
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OM protein - protein_search, using sw model

Run on: September 18, 2002, 15:15:32 ; Search time 28.8 Seconds
(Without alignments)
168.774 Million cell updates/sec

Title: US-09-383-551B-2
Perfect score: 1082
Sequence: 1 MKSLWFFFLCRLIKVLGT.....YMFRAVNTAKKSLTDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	15.1	218	3	US-08-228-208A-20
2	146.5	13.5	225	1	US-08-505-058-4
3	146.5	13.5	225	2	US-08-459-818-24
4	146.5	13.5	225	2	US-08-889-666-24
5	146.5	13.5	225	2	US-08-465-078-24
6	146.5	13.5	225	2	US-08-725-776-24
7	146.5	13.5	225	2	US-08-488-062-24
8	140	12.9	218	3	US-08-228-208A-19
9	134.5	12.4	220	3	US-08-228-208A-21
10	134	12.4	225	1	US-08-505-058-3
11	134	12.4	225	2	US-08-459-818-23
12	134	12.4	225	2	US-08-889-666-23
13	134	12.4	225	2	US-08-465-078-23
14	134	12.4	225	2	US-08-725-776-23
15	134	12.4	225	2	US-08-488-062-23
16	126	11.6	223	1	US-08-505-058-5
17	126	11.6	223	2	US-08-459-818-25
18	126	11.6	223	2	US-08-889-666-25
19	126	11.6	223	2	US-08-465-078-25
20	126	11.6	223	2	US-08-725-776-25
21	126	11.6	223	2	US-08-488-062-25
22	120.5	11.1	367	3	US-08-630-172-19
23	120.5	11.1	367	4	US-09-375-419-19
24	119.5	11.0	134	3	US-08-630-172-3
25	119.5	11.0	134	4	US-09-375-419-3
26	110.5	10.2	110	4	US-09-460-384-33
27	93	8.6	221	3	US-08-228-208A-22

28	89.5	8.3	117	2	US-08-529-878B-39	Sequence 39, Appl
29	87	8.0	330	2	US-08-332-562A-81	Sequence 81, Appl
30	87	8.0	330	2	US-08-332-562A-134	Sequence 134, App
31	86.5	8.0	209	4	US-09-430-503-20	Sequence 20, Appl
32	84.5	7.8	209	4	US-09-430-503-18	Sequence 18, Appl
33	84.5	7.8	209	4	US-09-430-503-24	Sequence 24, Appl
34	84	7.8	223	3	US-08-228-208A-17	Sequence 17, Appl
35	84	7.8	283	2	US-08-332-562A-136	Sequence 136, App
36	82.5	7.6	209	4	US-09-430-503-22	Sequence 22, Appl
37	81.5	7.5	187	1	US-08-067-684-14	Sequence 14, Appl
38	81.5	7.5	187	1	US-08-008-898-14	Sequence 14, Appl
39	81.5	7.5	187	2	US-08-459-818-14	Sequence 14, Appl
40	81.5	7.5	187	2	US-08-889-666-14	Sequence 14, Appl
41	81.5	7.5	187	2	US-08-465-078-14	Sequence 14, Appl
42	81.5	7.5	187	2	US-08-725-776-14	Sequence 14, Appl
43	81.5	7.5	187	2	US-08-488-062-14	Sequence 14, Appl
44	81.5	7.5	187	3	US-08-228-208A-14	Sequence 14, Appl
45	81.5	7.5	187	5	PCT-US95-06726-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-228-208A-20
; Sequence 20, Application US/08228208A
; Patent No. 6090914
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Wallace, Philip M.
; TITLE OF INVENTION: CTLA4/CD28ig HYBRID FUSION
; TITLE OF INVENTION: PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,208A
; FILING DATE: 15-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-30US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310 445-1140
; TELEFAX: 310 445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-228-208A-20

Query Match 15.1%; Score 163; DB 3; Length 218;
Best Local Similarity 26.5%; Pred. No. 3e-11;
Matches 41; Conservative 31; Mismatches 65; Indels 18; Gaps 7;

QY 30 MFEHNGGVQILCKYPD--IVQOFKQMLKGGQILCDLTKTKGSGNVTISKSLK-----F 82
DB 29 LLVYDNEVSLSCRYSYNLLAKEFRASLYKG--VNSDVEVCVGNFTYQOPQFRPNVGN 86
QY 83 CHSOLSNNSVSFFLYNLDHSHANYFCNLSIFDPPPF--KVTLTGGYLHIYESOLC---C 137
DB 87 CCGNFDETVTFRLWLDVNHHTDIYFCKIEVMPYPYLDNEKSNGTIIHIKEKHLCCHAQT 146
QY 138 QLKFWLPICGAFFVVC--ILGCILIC--WLTKKK 168
DB 147 SPKLEWPLVVAGVLLCYGLLYTTLCTIITNSRR 181

RESULT 2
US-08-505-058-4
Sequence 4, Application US/08505058
Patent No. 5773253
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Peach, Robert
TITLE OF INVENTION: CTLA4 Mutant Molecules and Uses Thereof
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 15-APR-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/505,058
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.30US11
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-505-058-4

Query Match 13.5%; Score 146.5; DB 1; Length 225;
Best Local Similarity 26.2%; Pred. No. 2.7e-09;
Matches 42; Conservative 31; Mismatches 64; Indels 23; Gaps 9;

QY 30 MFEHNGGVQILCKYPD--IVQOFKQMLKGGQILCDLTKTKGSGNVTISKSLK---- 81
DB 30 LLVYDNEVSLSCRYSYNLLAKEFRASLYKG--VNSDVEVCVGNFTYQOPQFRPNVG 87

Query Match 13.5%; Score 146.5; DB 2; Length 225;
Best Local Similarity 26.2%; Pred. No. 2.7e-09;
Matches 42; Conservative 31; Mismatches 64; Indels 23; Gaps 9;

QY 30 MFEHNGGVQILCKYPD--IVQOFKQMLKGGQILCDLTKTKGSGNVTISKSLK---- 81
DB 30 LLVYDNEVSLSCRYSYNLLAKEFRASLYKG--VNSDVEVCVGNFTYQOPQFRPNVG 87

Query Match 13.5%; Score 146.5; DB 2; Length 225;
Best Local Similarity 26.2%; Pred. No. 2.7e-09;
Matches 42; Conservative 31; Mismatches 64; Indels 23; Gaps 9;

QY 30 MFEHNGGVQILCKYPD--IVQOFKQMLKGGQILCDLTKTKGSGNVTISKSLK---- 81
DB 30 LLVYDNEVSLSCRYSYNLLAKEFRASLYKG--VNSDVEVCVGNFTYQOPQFRPNVG 87

QY 82 -FCHSOLSNNSVSFFLYNLDHSHANYFCNLSIFDPPPF--KVTLTGGYLHIYESOLC--- 136
DB 88 FNCNDFNDETVTFRLWLDVNHHTDIYFCKIEVMPYPYLDNEKSNGTIIHIKEKHLCCHA 147
QY 137 ----COLKFWLPICGAFFVVC--ILGCILIC--WLTKKK 168
DB 148 XXXQTSPLKFWPLVVAGVLLCYGLLYTTLCTIITNSRR 187

RESULT 3
US-08-459-818-24
Sequence 24, Application US/08459818
Patent No. 5851795
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,818
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.35US02
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-818-24

Query Match 13.5%; Score 146.5; DB 2; Length 225;
Best Local Similarity 26.2%; Pred. No. 2.7e-09;
Matches 42; Conservative 31; Mismatches 64; Indels 23; Gaps 9;

QY 30 MFEHNGGVQILCKYPD--IVQOFKQMLKGGQILCDLTKTKGSGNVTISKSLK---- 81
DB 30 LLVYDNEVSLSCRYSYNLLAKEFRASLYKG--VNSDVEVCVGNFTYQOPQFRPNVG 87

QY 82 -FCHSOLSNNSVSFFLYNLDHSHANYFCNLSIFDPPPF--KVTLTGGYLHIYESOLC--- 136
DB 88 FNCNDFNDETVTFRLWLDVNHHTDIYFCKIEVMPYPYLDNEKSNGTIIHIKEKHLCCHA 147

QY 137 ----COLKFWLPICGAFFVVC--ILGCILIC--WLTKKK 168
DB 148 XXXQTSPLKFWPLVVAGVLLCYGLLYTTLCTIITNSRR 187

RESULT 4
US-08-899-666-24
Sequence 24, Application US/08899666

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:16:17 ; Search time 37.55 Seconds
(without alignments)
509.235 Million cell updates/sec

Title: US-09-383-551B-2
Perfect score: 1082
Sequence: 1 MKSGLWYFFLCLIRKVLGT.....YMFRAVNTAKKSLTDTVL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1082	100.0	199	2 S78540	inducible T-cell c
2	701	64.8	200	2 JC7397	activation-inducib
3	696	64.3	216	2 JC7396	activation-inducib
4	152	14.0	218	2 S24113	T-cell surface gly
5	150.5	13.9	221	2 I46689	CD28 precursor - r
6	139.5	12.9	173	2 I46197	cell surface prote
7	139.5	12.9	220	1 RWHU28	T-cell surface gly
8	138	12.8	218	2 A43523	T-cell surface gly
9	103.5	9.6	988	2 T18986	hypothetical prote
10	97	9.0	221	2 S25168	CHT28 protein - ch
11	91.5	8.5	383	2 T21946	hypothetical prote
12	87	8.0	330	2 A40071	Fc gamma (IgG) rec
13	87	8.0	330	2 I49660	Fc-gamma-1/gamma-2
14	87	8.0	563	2 T32479	hypothetical prote
15	86.5	8.0	223	2 A29063	cytotoxic T-lympho
16	86	7.9	223	2 T09536	cytotoxic T-lympho
17	84	7.8	283	1 FCMSG1	Fc gamma (IgG) rec
18	84	7.8	285	2 D69440	conserved hypotet
19	83.5	7.7	186	2 S08614	cytotoxic T-lympho
20	82.5	7.6	248	1 QBE4L	probable glycoprot
21	81	7.5	276	2 S20690	31.6K hypothetical
22	81	7.5	680	2 JC5895	killer cell inhibi
23	81	7.5	1584	2 S57161	hypothetical prote
24	80.5	7.4	247	2 D90028	hypothetical prote
25	80.5	7.4	635	2 JC5896	killer cell inhibi
26	78	7.2	231	2 T23136	hypothetical prote
27	77.5	7.2	80	2 F86027	hypothetical prote
28	77.5	7.2	220	2 A48581	37K proline-rich s
29	77.5	7.2	1070	2 JC4593	protein-tyrosine k

30	77	7.1	338	2 T34364	hypothetical prote
31	77	7.1	2104	2 D81286	hypothetical prote
32	77	7.1	2104	2 H86127	hypothetical prote
33	76.5	7.1	223	2 I46696	CTLA-4 precursor -
34	76.5	7.1	323	2 S06946	Fc gamma (IgG) rec
35	76.5	7.1	1237	2 A54080	protein-tyrosine-p
36	76	7.0	301	2 I54209	hypothetical prote
37	76	7.0	317	2 J10118	Fc gamma (IgG) rec
38	76	7.0	546	2 S22053	cytochrome-c oxida
39	75.5	7.0	261	2 S29360	Fc gamma (IgG) rec
40	75.5	7.0	277	2 T21330	hypothetical prote
41	75.5	7.0	2135	2 T14602	variant-specific s
42	75	6.9	418	2 AD3417	transporter, mfs s
43	75	6.9	1132	1 QSBPL	host specificity p
44	74.5	6.9	201	2 G90134	hypothetical prote
45	74.5	6.9	235	2 I50610	T-cell surface gly

ALIGNMENTS

RESULT 1

S78540
inducible T-cell co-stimulator ICOS precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 07-May-1999
C:Accession: S78540; S78748; S78749
R.Kroczek, R.
submitted to the Protein Sequence Database, June 1998
A:Reference number: S78540
A:Accession: S78540
A:Molecule type: mRNA
A:Residues: 1-199 <KRO>
A:Experimental source: cell line MOLT-4V
R.Hutloff, A.; Dittlich, A.M.; Beier, K.C.; Eljaschewitsch, B.; Kraft, R.; Anagnostop
Nature 397, 263-266, 1999
A:Title: ICOS is an inducible T-cell co-stimulator structurally and functionally rela
A:Reference number: S78748; MUID:99127892
A:Accession: S78748
A:Molecule type: mRNA
A:Residues: 1-199 <HUT1>
A:Experimental source: cell line MOLT-4V
A:Accession: S78749
A:Molecule type: protein
A:Residues: 'X', 193-198 <HUT2>
A:Experimental source: cell line MOLT-4V
C:Complex: homodimer
C:Superfamily: immunoglobulin homology
C:Keywords: dimer; glycoprotein; T-cell; transmembrane protein
F:1-19/Domain: (or 1-20) signal sequence #status predicted <SIG>
F:20-199/Product: (or 21-199) inducible costimulator ICOS #status predicted <MAT>
F:21-138/Domain: extracellular #status predicted <EXT>
F:26-132/Domain: immunoglobulin homology <IMM>
F:139-164/Domain: transmembrane #status predicted <TM>
F:165-199/Domain: intracellular #status predicted <INT>
F:23,89,110/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1082; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.1e-97;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	MKSGLWYFFLCLIRKVLGTGEINGSANYEMFIFHNGGVQILCKYPDIVOQFKMOLLKGQ	60
Db	1	MKSGLWYFFLCLIRKVLGTGEINGSANYEMFIFHNGGVQILCKYPDIVOQFKMOLLKGQ	60
Oy	61	ILCDLTTKTGGNTVSIKSKFCHSOLSNNVSFFLYNLDHSHANYFCNLSIFDPPPPK	120
Db	61	ILCDLTTKTGGNTVSIKSKFCHSOLSNNVSFFLYNLDHSHANYFCNLSIFDPPPPK	120
Oy	121	VLTGGLYHIESQLCCQLKFWLPICGAFAFVVCVVCILGICILICWLTKKKYSSSVHPDNGEY	180
Db	121	VLTGGLYHIESQLCCQLKFWLPICGAFAFVVCVVCILGICILICWLTKKKYSSSVHPDNGEY	180

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:25:12 ; Search time 20.28 Seconds
(without alignments)
379.940 Million cell updates/sec

Title: US-09-383-551B-2

Perfect score: 1082

Sequence: 1 M K S G L N Y F F L C L R I K V L T G Y M F M R A V N T A K K S R L T D V I L 199

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	159	14.7	218	1	CD28_RAT
2	150.5	13.9	221	1	CD28_RABIT
3	141	13.0	219	1	CD28_BOVIN
4	139.5	12.9	220	1	CD28_HUMAN
5	138	12.8	218	1	CD28_MOUSE
6	97	9.0	221	1	CD28_CHICK
7	89	8.2	321	1	OSV1_HUMAN
8	87	8.0	330	1	FCG2_MOUSE
9	86.5	8.0	223	1	CTL4_MOUSE
10	86	7.9	223	1	CTL4_HUMAN
11	82.5	7.6	248	1	VGL2_EBV
12	81	7.5	1382	1	MET_RAT
13	81	7.5	1584	1	YJ9G_YEAST
14	77.5	7.2	324	1	CRFB_SHEEP
15	77.5	7.2	1070	1	PRK7_HUMAN
16	76.5	7.1	223	1	CD28_RABIT
17	76.5	7.1	323	1	FCG3_HUMAN
18	76	7.0	317	1	FCGA_HUMAN
19	76	7.0	448	1	BCN1_MOUSE
20	76	7.0	450	1	BCN1_HUMAN
21	76	7.0	466	1	ALAA_RABIT
22	76	7.0	562	1	ADAD_MOUSE
23	75.5	7.0	261	1	FCG3_MOUSE
24	75	6.9	462	1	CATC_MOUSE
25	75	6.9	1132	1	VHSJ_LAMBDA
26	74.5	6.9	761	1	AD24_MOUSE
27	74	6.8	344	1	OM40_DRONE
28	74	6.8	367	1	NULM_PODAN
29	73.5	6.8	285	1	FCG2_RAT
30	73.5	6.8	322	1	CRFB_MOUSE
31	73.5	6.8	360	1	CCPH_HSVSA
32	73.5	6.8	496	1	GRB_MOUSE
33	73.5	6.8	496	1	GRB_RAT

Query Match 14.7%; Score 159; DB 1; Length 218;
Best Local Similarity 26.5%; Pred. No. 2.1e-08;

ALIGNMENTS

RESULT 1

CD28_RAT 1
ID CD28_RAT STANDARD; PRT; 218 AA.
AC P31042;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T-cell-specific surface glycoprotein CD28 precursor.
GN CD28.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DA; TISSUE=Lymphoid;
RX MEDLINE=92104640; PubMed=1309509;
RT Clark G.J., Dallman M.J.;
RL "Identification of a cDNA encoding the rat CD28 homologue.";
CC Immunogenetics 35:54-57(1992).
CC -!- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1 AND B7-2 (B70).
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN

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EMBL; X55288; CAA39003.1; -;
PIR; S38722; S38722.
InterPro; IPR003600; Ig_Like.
DR SMART; SM00410; Ig_Like; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 218 T-CELL-SPECIFIC SURFACE GLYCOPROTEIN CD28.
FT DOMAIN 20 150 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 151 177 POTENTIAL.
FT DOMAIN 178 218 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 29 138 IG-LIKE V-TYPE DOMAIN.
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 218 AA; 25170 MW; 2E1518CF324C0B6E CRC64;

34 73.5 6.8 497 1 GRB_HUMAN P48167 homo sapien
35 73.5 6.8 1162 1 BXB_CLOBU Q08366 clostridium
36 73 6.7 275 1 YD84_YEAST Q12359 saccharomyc
37 73 6.7 916 1 SCRB_LIMPO Q25386 limulus pol
38 72.5 6.7 654 1 BFR2_HUMAN Q01742 homo sapien
39 72 6.7 561 1 AIAD_RAT P23944 rattus norv
40 72 6.7 569 1 YL53_YEAST Q06567 saccharomyc
41 71.5 6.6 634 1 YCX3_EUGR P31916 euglena gra
42 71.5 6.6 1051 1 PK7_CHICK Q91048 gallus gall
43 71 6.6 212 1 KITH_ENCCU Q06720 encephalito
44 71 6.6 466 1 AIAA_BOVIN P18130 bos taurus
45 70.5 6.5 524 1 VLL_HPV58 P26535 human papil

Matches 41; Conservative 30; Mismatches 66; Indels 18; Gaps 7;

QY 30 MFIFHNGVQILCKYPD--IVQOFKMLLKGQILCDLTKGSGNTVSIKSLK-----F 82
 Db 29 LLVVDNNEVSLSCRYSYNLLAKERASLYKG--VNSDEVCGVNGNFTYQPOFRPNVGN 86
 QY 83 CHISQLSNNSVFFLYNLDHSHANYFCNLISFDPPPF--KVTLTGGYLHIYESQLC---C 137
 Db 87 CDGDFNFTVTFRLNLDVNHHTDIYFCKIEVMYPPPYLDNEKSNGTIIHKEKHLCHAQT 146
 QY 138 OLKFWLPICAAFFVVC--ILGCILC--WLTKKK 168
 Db 147 SPKLFVPLVVAGVLLCYGLLVTLVLCIITWNSRR 181

RESULT 2

CD28_RABIT
 ID CD28_RABIT STANDARD; PRT; 221 AA.
 AC P42069;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 01-MAR-2002 (Rel. 41, Last annotation update)
 DE T-cell-specific surface glycoprotein CD28 precursor.
 GN CD28.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B/J X CHBB:HM;
 RX MEDLINE=95369849; PubMed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules.";
 RL Immunogenetics 42:217-220(1995).
 CC -!- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
 CC AND B7-2 (B70).
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC
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 CC -----

DR EMBL; D49841; BAA08641.1; .
 DR InterPro; IPR003600; Ig_Like.
 DR SMART; SM00410; IG_Like; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 19
 FT CHAIN 20 221
 FT
 FT DOMAIN 20 150
 FT TRANSMEM 151 177
 FT DOMAIN 178 221
 FT DOMAIN 29 138
 FT CARBOHYD 38 72
 FT CARBOHYD 72 72
 FT CARBOHYD 93 93
 FT CARBOHYD 106 106
 FT CARBOHYD 130 130
 FT CARBOHYD 221 AA; 25307 MW; 3DF652C9FC14F13 CRC64;
 SQ SEQUENCE

Query Match 13.9%; Score 150.5; DB 1; Length 221;
 Best Local Similarity 23.8%; Pred. No. 1.4e-07;
 Matches 38; Conservative 27; Mismatches 70; Indels 25; Gaps 6;

QY 30 MFIFHNGVQILCKYPD--IVQOFKMLLKGQILCDLTKGSGNTVSIKSLK-----GNTVSIKSL 80
 Db 29 LLVVDNNEVSLSCRYSYNLLAKERASLYKG--VNSDEVCGVNGNFTYQPOFRPNVGN 86
 QY 81 KECHSOLSNNSVFFLYNLDHSHANYFCNLISFDPPPF--KVTLTGGYLHIYESQLC--- 136
 Db 87 --CDKLGNETVTFYLNLDVNHHTDIYFCKIEVMYPPPYLDNEKSNGTIIHKEKHLCHAQT 144
 QY 137 -----COLKFWLPICAAFFVVC--ILGCILC--WLTKKK 168
 Db 145 HPSKSSSLFVWLVVGVAVLAFYSMLVTVALFSCWMSKK 184

RESULT 3

CD28_BOVIN
 ID CD28_BOVIN STANDARD; PRT; 219 AA.
 AC Q28071;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 01-MAR-2002 (Rel. 41, Last annotation update)
 DE T-cell-specific surface glycoprotein CD28 precursor.
 GN CD28.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96186531; PubMed=8606060;
 RA Parsons K.R., Young J.R., Collins R.A., Howard C.J.;
 RT "Cattle CTLA-4, CD28 and chicken CD28 bind CD86: MYPPPY is not
 RT conserved in cattle CD28.";
 RL Immunogenetics 43:388-391(1996).
 CC -!- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
 CC AND B7-2 (B70).
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC
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 CC -----

DR EMBL; X93304; CAA63707.1; .
 DR InterPro; IPR003600; Ig_Like.
 DR SMART; SM00410; IG_Like; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 18
 FT CHAIN 19 219
 FT
 FT DOMAIN 19 151
 FT TRANSMEM 152 178
 FT DOMAIN 179 219
 FT DOMAIN 28 136
 FT CARBOHYD 37 71
 FT CARBOHYD 71 71
 FT CARBOHYD 84 84
 FT CARBOHYD 91 91
 FT CARBOHYD 104 104
 FT CARBOHYD 128 128
 FT CARBOHYD 219 AA; 25143 MW; 85B5C650E96634AA CRC64;
 SQ SEQUENCE

Query Match 13.0%; Score 141; DB 1; Length 219;
 Best Local Similarity 23.2%; Pred. No. 1.2e-06;
 Matches 36; Conservative 32; Mismatches 71; Indels 16; Gaps 6;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:26:32 ; Search time 63.42 Seconds
(without alignments)
542.825 Million cell updates/sec

Title: US-09-383-551B-2
Perfect score: 1082
Sequence: 1 MKSGLWYFFLCLRIKVLTG.....YMFRAVNTAKSRLTDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1082	100.0	199	4 Q9Y6W8	Q9Y6W8 homo sapien
2	737.5	68.2	200	11 Q9WVS0	Q9WVS0 mus musculus
3	734	67.8	200	11 Q9JL17	Q9JL17 mus musculus
4	701	64.8	200	11 Q9RLT7	Q9RLT7 rattus norv
5	696	64.3	216	11 Q9WVR9	Q9WVR9 rattus norv
6	146.5	13.5	221	11 Q9JLV4	Q9JLV4 marmota mon
7	145.5	13.4	221	6 Q9N214	Q9N214 felis silve
8	145.5	13.4	221	6 Q02757	Q02757 felis silve
9	145	13.4	219	6 Q97630	Q97630 ovis aries
10	140.5	13.0	221	6 Q9GKP3	Q9GKP3 canis fami
11	140.5	13.0	221	6 Q9N0N8	Q9N0N8 canis fami
12	139.5	12.9	173	6 Q28289	Q28289 canis fami
13	136.5	12.6	220	6 Q9BDM8	Q9BDM8 macaca neme
14	135.5	12.5	220	6 Q9BDN5	Q9BDN5 cercocebus
15	130.5	12.1	220	6 Q9BDM6	Q9BDM6 macaca mula
16	125.5	11.6	220	6 Q9BDN8	Q9BDN8 papio anubi

17	115.5	10.7	220	6 Q9BDN2	Q9BDN2 callithrix
18	103.5	9.6	988	5 Q17710	Q17710 caenorhabdi
19	91.5	8.5	485	5 Q20139	Q20139 caenorhabdi
20	87	8.0	223	6 Q9BDP1	Q9BDP1 aotus trivi
21	84.5	7.8	209	4 Q9NYK4	Q9NYK4 homo sapien
22	84.5	7.8	223	11 Q9QZ27	Q9QZ27 mus musculu
23	84	7.8	223	4 Q96P43	Q96P43 homo sapien
24	84	7.8	285	17 Q28747	Q28747 archaeglob
25	84	7.8	419	13 Q9IA91	Q9IA91 morone saxa
26	83.5	7.7	223	11 Q9JLV3	Q9JLV3 marmota mon
27	83	7.7	1239	10 Q9FHM1	Q9FHM1 arabidopsis
28	82.5	7.6	223	11 Q62859	Q62859 rattus norv
29	82	7.6	223	6 Q9BDC4	Q9BDC4 macaca mula
30	82	7.6	223	6 Q9BDM7	Q9BDM7 papio anubi
31	81	7.5	276	12 Q98822	Q98822 human adeno
32	81	7.5	276	12 Q64861	Q64861 human adeno
33	81	7.5	680	11 Q55001	Q55001 mus musculu
34	80.5	7.4	247	16 Q99RX6	Q99RX6 staphylococ
35	80.5	7.4	635	11 Q55002	Q55002 mus musculu
36	80.5	7.4	663	11 Q70434	Q70434 mus musculu
37	79.5	7.3	269	4 Q95297	Q95297 homo sapien
38	79	7.3	370	4 Q9BZW8	Q9BZW8 homo sapien
39	78.5	7.3	310	11 Q9EQ87	Q9EQ87 mus musculu
40	78	7.2	231	5 Q45668	Q45668 caenorhabdi
41	77.5	7.2	311	11 Q9EQ86	Q9EQ86 mus musculu
42	77	7.1	323	6 Q9BDM2	Q9BDM2 cercopithec
43	77	7.1	338	5 Q22576	Q22576 caenorhabdi
44	77	7.1	539	12 P88842	P88842 avian infec
45	77	7.1	619	10 Q9XGG1	Q9XGG1 sorghum bic

ALIGNMENTS

RESULT 1

Q9Y6W8 PRELIMINARY; PRT; 199 AA.

ID Q9Y6W8; PRT; 199 AA.

AC Q9Y6W8; PRT; 199 AA.

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM

DE PRECURSOR (INDUCIBLE T-CELL CO-STIMULATOR PRECURSOR) (INDUCIBLE

DE COSTIMULATOR PRECURSOR).

GN ICOS.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BLOOD;

RA Tezuka K., Tamatani T.;

RT "Cell surface molecule mediating cell adhesion and signal

RT transmission.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99127892; PubMed=9930702;

RA Hutloff A., Dittlich A.M., Beier K.C., Eljaschewitsch B., Kraft R.,

RA Agnostonopoulos I., Kroczeck R.A.;

RT "ICOS is an inducible T-cell co-stimulator structurally and

RT functionally related to CD28.";

RL Nature 397:263-266(1999).

RN [3]

RP SEQUENCE FROM N.A.

RA Beier K.C., Hutloff A., Dittlich A.M., Heuck C., Mages H.W.,

RA Buechner K., Henn V., Rauch A., Kroczeck R.A.;

RT "Detailed analysis of human ICOS and its ligand.";

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=THYMUS;

RX MEDLINE-20243570;
RA Aicher A., Hayden-Ledbetter M., Brady W.A., Pezzutto A., Richter G.,
RA Magaletti D., Buckwalter S., Ledbetter J.A., Clark E.A.;
RT "Characterization of human inducible costimulator ligand expression
and function.";
RL J. Immunol. 164:4689-4696(2000).
DR EMBL; AB023135; BAA82129.1; -;
DR EMBL; AJ277832; CAC06612.1; -;
DR EMBL; AF218312; AAF71301.1; -;
KW SIGNAL. 1 20 POTENTIAL.
FT SIGNAL. 1 20 POTENTIAL.
SQ SEQUENCE 199 AA; 22624 MW; 214EC741C9BDC9FC CRC64;

Query Match 100.0%; Score 1082; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 2.8e-109; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0;

Qy 1 MKSGLWYFFFLCRLIKVLTGEINGSANYEMFIFHNGGVQIILCKYDPDIQQFKMQLLKGQ 60
1 MKSGLWYFFFLCRLIKVLTGEINGSANYEMFIFHNGGVQIILCKYDPDIQQFKMQLLKGQ 60
61 ILCDLTKTGSGNTVSIKSLKFCCHSOLSNNSVSFFLYNLDHSHANYFCNLISIFDPPPPK 120
61 ILCDLTKTGSGNTVSIKSLKFCCHSOLSNNSVSFFLYNLDHSHANYFCNLISIFDPPPPK 120
Qy 121 VLTGGYLHIYESOLCCOLKFWLPICGAFFVVCILGCLICWLTKKYSVVHDPNGEY 180
121 VLTGGYLHIYESOLCCOLKFWLPICGAFFVVCILGCLICWLTKKYSVVHDPNGEY 180
Db 121 VLTGGYLHIYESOLCCOLKFWLPICGAFFVVCILGCLICWLTKKYSVVHDPNGEY 180
Qy 181 MFMAVNTAKKSLRLDVT 199
181 MFMAVNTAKKSLRLDVT 199

RESULT 2
Q9WVS0 PRELIMINARY; PRT; 200 AA.
AC Q9WVS0;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
DE PRECURSOR (CCLP PRECURSOR) (SURFACE PROTEIN).
GN CCLP OR ICOS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Tezuka K., Tamatani T.;
RT "Cell surface molecule mediating cell adhesion and signal
transmission.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Wu D., Giannoni M.A., Kiesecker C.L., Faas S.J., Mickle A.P.,
RA Matis L.A., Rother R.P.;
RT "CCLP, A novel molecule that regulates T cell activation.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RX MEDLINE-20225659; PubMed=10760791;
RA Mages H.W., Hutloff A., Heuck C., Buchner K., Himmelbauer H.,
RA Oliveri F., Kroccek R.A.;
RT "Molecular cloning and characterization of murine ICOS and
its ligand.";
RL Immunol. 30:1040-1047(2000).
[3]
RX MEDLINE-20243570; BAA82126.1; -;

DR EMBL; AF257230; AAF70099.1; -;
DR EMBL; AJ250559; CAB71153.1; -;
DR MGD; MGI:1858745; ICOS.
KW SIGNAL. 1 20 POTENTIAL.
FT SIGNAL. 1 20 POTENTIAL.
SQ SEQUENCE 200 AA; 22690 MW; 9B2278E4CAB1DB47 CRC64;

Query Match 68.2%; Score 737.5; DB 11; Length 200;
Best Local Similarity 69.3%; Pred. No. 6e-72; Indels 1; Gaps 1;
Matches 138; Conservative 20; Mismatches 40;

Qy 1 MKSGLWYFFFLCRLIKVLTGEINGSANYEMFIFHNGGVQIILCKYDPDIQQFKMQLLKGQ 60
1 MKSGLWYFFFLCRLIKVLTGEINGSANYEMFIFHNGGVQIILCKYDPDIQQFKMQLLKGQ 60
61 ILCDLTKTGSGNTVSIKSLKFCCHSOLSNNSVSFFLYNLDHSHANYFCNLISIFDPPPPK 120
61 ILCDLTKTGSGNTVSIKSLKFCCHSOLSNNSVSFFLYNLDHSHANYFCNLISIFDPPPPK 120
Qy 121 V-TLGGYLHIYESOLCCOLKFWLPICGAFFVVCILGCLICWLTKKYSVVHDPNGE 179
121 ERNLSGGYLHIYESOLCCOLKFWLPICGAFFVVCILGCLICWLTKKYSVVHDPNGE 180
Db 180 YMFRAVNTAKKSLRLDVT 198
180 YMFRAVNTAKKSLRLDVT 198
Qy 181 YMFMAVNTAKKSLRLAGVT 199
181 YMFMAVNTAKKSLRLAGVT 199

RESULT 3
Q9JLI7 PRELIMINARY; PRT; 200 AA.
AC Q9JLI7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CD28-RELATED PROTEIN 1 (INDUCIBLE COSTIMULATORY PROTEIN)
DE (FRAGMENT).
GN ICOS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINAL INTRA-EPITHELIUM;
RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
RA Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tafuri-Bladt A.,
RA Campbell P., Chang D., Chiu L., Bai T., Duncan G., Elliott G.S.,
RA Hui A., McCabe S.M., Scully S., Shaklee C.L., Van G., Mak T.W.,
RA Senaldi G.;
RT "T-cell co-stimulation through B7RP-1 and ICOS.";
RL Nature 0:0-0(2000).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=129/OLA;
RA McAdam A.J., Greenwald R.J., Levin M.A., Chernova T., Malenkovich N.,
RA Ling V., Freeman G.J., Sharpe A.H.;
RT "The inducible costimulatory (ICOS) molecule is critical for CD40-
mediated antibody class switching.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216748; AAF45150.1; -;
DR EMBL; AF327185; AAG48732.1; -;
DR EMBL; AF327184; AAG48732.1; JOINED.
FT NON_TER 200
SQ SEQUENCE 200 AA; 22709 MW; 87D97F0DC44ADCA7 CRC64;

Query Match 67.8%; Score 734; DB 11; Length 200;
Best Local Similarity 70.4%; Pred. No. 1.4e-71;
Matches 138; Conservative 19; Mismatches 35; Indels 4; Gaps 2;

Qy 7 YF---FLFLCRLIKVLTGEINGSANYEMFIFHNGGVQIILCKYDPDIQQFKMQLLKGQILC 63


```
QY 74 TVSIKSLKF-----CHSLSNNSVSFFLYNLDHSHANYFCNLSIFDPPPF--KVLTIT 124
Db 75 ----HQLQFYSGTGCNCDKLGNETVTFYLRNLYVNTQDIYFCKIEVMPYPPYLDNKS 130
QY 125 GGYLHIYESQLCCQ-----KFW-LPIGCAAFVVCVILCGILICWLTKKYSSSVHDP 176
Db 131 GTVIHVKNENICPGVPSPKPFMTLVVFGVLGIYSLLSMTLLCYLWTKRQTRL--L 188
QY 177 NGEYMF 183
Db 189 QSDYNNM 195

RESULT 7
Q9N2I4 PRELIMINARY; PRT; 221 AA.
AC Q9N2I4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
CD28.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20094001; PubMed=10630305;
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
RA Mikami T., Takahashi E.;
RT "Molecular cloning and sequencing of a cDNA encoding the feline T-cell
RT antigen CD28 homologue.";
RL Immunogenetics 50:369-370(1999).
DR EMBL; AB025316; BAA92349.1; -.
DR InterPro; IPR003600; Ig_like.
DR SMART; SM00410; Ig_like.1.
SQ SEQUENCE 221 AA; 25283 MW; B17B76C52BA18DCB CRC64;
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Query Match 13.4%; Score 145.5; DB 6; Length 221;
Best Local Similarity 28.38; Pred. No. 9.8e-08;
Matches 45; Conservative 22; Mismatches 65; Indels 27; Gaps 8;

QY 32 IFHNGGVQILCKYPD--IVQQFKMQLLKGQILCDLTKTG--SGNTVSIKSLKF-CHSQ 86
Db 31 VVYNNEVLNLSCKYTHNFSKEFRASLYKGVDSAVECVVNGYSHQPFYSTGDCDGK 90

QY 87 LSNNVSFFLYNLDHSHANYFCNLSIFDPPPF--KVLTGTGGLHIYESQLC-COLK--- 140
Db 91 LGNETVTFYLRNLFVNQTDIYFCKIEVMPYPPYIDNEKSNGTIIHVKEKHLCPAQLSPES 150

QY 141 ---FWLPIGCAAFVVCVILG-----CILICWLTKKK 168
Db 151 SKPFW-----ALVVVGILGFYSLLATVALGACWMTKR 184

Query Match 13.4%; Score 145.5; DB 6; Length 221;
Best Local Similarity 28.38; Pred. No. 9.8e-08;
Matches 45; Conservative 22; Mismatches 65; Indels 27; Gaps 8;

QY 32 IFHNGGVQILCKYPD--IVQQFKMQLLKGQILCDLTKTG--SGNTVSIKSLKF-CHSQ 86
Db 31 VVYNNEVLNLSCKYTHNFSKEFRASLYKGVDSAVECVVNGYSHQPFYSTGDCDGK 90

QY 87 LSNNVSFFLYNLDHSHANYFCNLSIFDPPPF--KVLTGTGGLHIYESQLC-COLK--- 140
Db 91 LGNETVTFYLRNLFVNQTDIYFCKIEVMPYPPYIDNEKSNGTIIHVKEKHLCPAQLSPES 150

QY 141 ---FWLPIGCAAFVVCVILG-----CILICWLTKKK 168
Db 151 SKPFW-----ALVVVGILGFYSLLATVALGACWMTKR 184

RESULT 8
O02757 PRELIMINARY; PRT; 221 AA.
ID O02757;
AC O02757;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE T-CELL SPECIFIC SURFACE GLYCOPROTEIN CD28.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Hash S.M., Carpino M.R., Collisson E.W.;
RT "Felis catus t-cell specific surface glycoprotein CD28.";
```

```
RL Thesis (1996), Veterinary Pathobiology, Texas A&M Univ.
DR EMBL; U57754; AAB53574.1; -.
DR InterPro; IPR003600; Ig_like.
DR SMART; SM00410; Ig_like.1.
SQ SEQUENCE 221 AA; 25317 MW; 5B71717E461AE5E3 CRC64;

Query Match 13.4%; Score 145.5; DB 6; Length 221;
Best Local Similarity 28.38; Pred. No. 9.8e-08;
Matches 45; Conservative 22; Mismatches 65; Indels 27; Gaps 8;

QY 32 IFHNGGVQILCKYPD--IVQQFKMQLLKGQILCDLTKTG--SGNTVSIKSLKF-CHSQ 86
Db 31 VVYNNEVLNLSCKYTHNFSKEFRASLYKGVDSAVECVVNGYSHQPFYSTGDCDGK 90

QY 87 LSNNVSFFLYNLDHSHANYFCNLSIFDPPPF--KVLTGTGGLHIYESQLC-COLK--- 140
Db 91 LGNETVTFYLRNLFVNQTDIYFCKIEVMPYPPYIDNEKSNGTIIHVKEKHLCPAQLSPES 150

QY 141 ---FWLPIGCAAFVVCVILG-----CILICWLTKKK 168
Db 151 SKPFW-----ALVVVGILGFYSLLATVALGACWMTKR 184

RESULT 9
O97630 PRELIMINARY; PRT; 219 AA.
ID O97630;
AC O97630;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE T-CELL SPECIFIC SURFACE GLYCOPROTEIN CD28.
GN CD28.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99309828; PubMed=10380709;
RA Chaplin P.J., Pietrala L.N., Scheerlinck J.P.;
RT "Cloning and sequence comparison of sheep CD28 and CTLA-4.";
RL Immunogenetics 49:583-584(1999).
DR EMBL; AF092739; AAD04379.1; -.
DR InterPro; IPR003600; Ig_like.
DR SMART; SM00410; Ig_like.1.
SQ SEQUENCE 219 AA; 25158 MW; D50AD339E5BC2327 CRC64;

Query Match 13.4%; Score 145; DB 6; Length 219;
Best Local Similarity 23.58; Pred. No. 1.1e-07;
Matches 40; Conservative 35; Mismatches 75; Indels 20; Gaps 8;

QY 30 MFIFHNGGVQILCKYPD--IVQQFKMQLLKGQILCDLTKTGSG--GNTVSIKSLKF-CHS 85
Db 28 MLVYNDNEVLNLSCKYTYNLFESKEFRASLYKGADSAVECAVNGNHSHPQLSTKNEFCNTV 87

QY 86 QLSNNSVSFFLYNLDHSHANYFCNLSIFDPPPF--KVLTGTGGLHIYESQLC----- 136
Db 88 KVGNETVTFYLRNLFVNQTDIYFCKIEVLPYPPYIDNEKSNGTIIHVKEKHLCPSPSPS 147

QY 137 COLKFWLPI---GCAAFVVCVILCGILICWLTKKYSSSVHDPNCEYMF 183
Db 148 SSKPFWALVVVGVVLFYSLVLTVALCNCWMTKR--NRMH--QSDYNNM 193

RESULT 10
O9GKP3 PRELIMINARY; PRT; 221 AA.
ID O9GKP3;
AC O9GKP3;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:26:25 ; Search time 75.12 Seconds
(without alignments)
295.724 Million cell updates/sec

Title: US-09-383-551B-13

Perfect score: 1070

Sequence: 1 MKPVSCVFVFCFLIKLTG.....YMFMAAVNTNKKSLRAGMTS 200

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

T number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1070	100.0	200	19 AAW71874	Rat cell surface p
2	1056	98.7	216	19 AAW71875	Rat cell surface p
3	922	86.2	200	21 AAB08723	Amino acid sequenc
4	922	86.2	200	21 AAY92212	Murine Th2-specifi
5	907	84.8	200	19 AAW75958	Mouse cell surface
6	701	65.5	199	19 AAW75956	Human cell surface
7	701	65.5	199	19 AAW75957	Human cell surface
8	701	65.5	199	20 AAY08026	Human activated T-
9	701	65.5	199	21 AAB08731	Amino acid sequenc
10	701	65.5	199	22 AAE03428	Human gene 2 encod
11	701	65.5	199	22 AAE03460	Human gene 2 encod

12	701	65.5	199	22 AAE03525	Human secreted pro
13	685.5	64.1	198	21 AAY92213	Human Th2-specific
14	552	51.6	380	22 AAB67717	Amino acid sequenc
15	430.5	40.2	379	22 AAB67716	Amino acid sequenc
16	141	13.2	220	13 AAR20805	Human CD28 antigen
17	141	13.2	220	13 AAR27103	Sequence encoded b
18	141	13.2	220	17 AAW02131	Human CD28 cDNA pr
19	141	13.2	220	17 AAR91433	Human CD28 antigen
20	141	13.2	220	18 AAW38413	CD28. Homo sapien
21	141	13.2	220	19 AAW80442	Human CD28 antigen
22	141	13.2	220	20 AAW88451	Human CD28 antigen
23	141	13.2	220	21 AAY96128	Human cell surface
24	141	13.2	220	21 AAY44294	Human CD28 recepto
25	141	13.2	220	22 AAU02437	Human lymphocyte c
26	130.5	12.2	223	20 AAY41137	Human CD28 protein
27	117	10.9	221	21 AAY32286	Feline CD28. Feli
28	117	10.9	221	21 AAY32279	Cat CD28 receptor.
29	116.5	10.9	134	18 AAR35846	Human CD28 for use
30	116.5	10.9	152	16 AAR67706	CD28 extracellular
31	112.5	10.5	367	18 AAW35862	Human CD28:IG2a c
32	108.5	10.1	225	20 AAY41136	Rat CD28 protein s
33	86	8.0	225	20 AAY41135	Mouse CD28 protein
34	82	7.7	244	20 AAY00161	Enterococcus faeca
35	82	7.7	269	20 AAY00160	Enterococcus faeca
36	82	7.7	503	22 AAB92984	Human protein sequ
37	81.5	7.6	117	20 AAY24469	Human CD28 gene pr
38	81.5	7.6	226	20 AAY41138	Chicken CD28 prote
39	77.5	7.2	964	21 AAB13634	C. trachomatis pmp
40	77.5	7.2	964	22 AAG83202	Protein encoded by
41	77.5	7.2	977	21 AAB13640	C. trachomatis pmp
42	77.5	7.2	977	22 AAG83208	Protein encoded by
43	76	7.1	223	21 AAY32287	Feline CTLA-4. Fe
44	76	7.1	223	21 AAY32280	Cat CTLA-4 recepto
45	76	7.1	803	13 AAR29030	Bacillus thuringie

ALIGNMENTS

RESULT 1

AAW71874
ID AAW71874 standard; Protein; 200 AA.
XX AAW71874;
AC
XX
DT 11-DEC-1998 (first entry)
XX
DE
DE
XX
KW Rat: cell surface protein; thymocyte; lymphocyte; cell adhesion;
KW signal transmission; autoimmune disorder; allergy; diagnosis;
KW mitogen-stimulated.
XX
OS Rattus sp.
XX
PN WO9838216-A1.
XX
PD 03-SEP-1998.
XX
PF 27-FEB-1998; 98WO-JP00837.
XX
PR 26-FEB-1998; 98JP-0062217.
XX
PR 27-FEB-1997; 97JP-0062290.
XX
(NISB) JAPAN TOBACCO INC.
XX
Tamatani T, Tezuka K;
XX
WPI; 1998-481144/41.
XX
N-PSDB; AAV61357.
XX

Cell surface molecule expressed in thymocytes and lymphocytes and - mediating signal transmission and cell adhesion, and antibodies to

PT it useful in treatment of auto:immune and allergic disorders.

Claim 9; Page 106-109; 149pp; Japanese.

The present sequence represents a rat cell surface protein which is expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell surface protein induces adhesion of mitogen-stimulated lymphocytes to antibodies recognising the cell surface protein. These antibodies also produce an increase in peripheral blood lymphocytes in the presence of an antibody recognising CD3 antigen. The cell surface protein contains the amino acid sequence FDPDPFF in its extracellular region and the sequence YWFM in its intracellular region. The cell surface protein can be used in the prevention and treatment of autoimmune and allergic diseases, and in the diagnosis and investigation of such disorders.

AA	Sequence	200 AA;
SQ		

Query Match	100.0%	Score 1070;	DB 19;	Length 200;
Best Local Similarity	100.0%	Pred. No. 2.3e-112;		
Matches 200; Conservative	0;	Mismatches	0;	Indels 0;

QY 1 MKPYFSCVFCFLIKLLTGELNDLANHRMFSFHDGGVQISCNYPETVQQKMKQLFKDRE 60

Db 1 mkpyfscvfcflkl1ltgelndlanhrmfsfhdqgqvaiscnyypetvqqlkmalfkdre 60

QY 61 VLCDLTKTGSGNTVSIKNPMSCPYQLSNNSVSFFLDNADSSQGSYFLCSLSIFDPPPPFO 120

Db 61 vlcdltktkqsgntvsi1knpmscpyqlsnnsvsffldnadssqqsvflcslsifdppppf 120

QY • 121 EKNLSGGYLLIYESQLCCQLKLWLPVGCAAFVAALLFGCIFI VWF AKKKYRSSVHDPNSE 180

Db 121 eknlsgqy1livesqlccqklwlpvqcaafvaallfqacifiwvfkakkyrsgsvhdpnse 180

Qy 181 YMFMAAVNTNKKSRLAGMTS 200

Db 181 ymfmaavntnkkxrlagmts 200

RESULT 2

AAW71875
ID AAW71875 standard; Protein; 216 AA.

AAW71875:

DT 11-DEC-1998 (first entry)

Rat cell surface protein #2.

Rat; cell surface protein; thymocyte; lymphocyte; cell adhesion;
 KW signal transmission; autoimmune disorder; allergy; diagnosis;
 KW mitogen-stimulated.

Rattus sp.

AX
PN
WO9838216-A1.

XX PD 03-SEP-1998.

XX 27-FEB-1998: 98WO-JP00837.

XX
PR 26-FEB-1998: 98JP-0062217

PR 27-FEB-1997; 97JP-0062290.
XX

PA (NISB) JAPAN TOBACCO INC.
XX

PI
YY
Tamatani T, Tezuka K;

DR WPI; 1998-481144/41.
DR N-PSDR: AA61359

XX
nm cell surface mole

PT mediating signal transmission and cell adhesion, and antibodies to

PR 03-FEB-1999; 99US-0244448.
PR 08-MAR-1999; 99US-0264527.
XX (AMGE-) AMGEN INC.
XX Yoshinaga SK;
XX WPI; 2000-543476/49.
DR N-PSDB; AAA64554.
XX Novel nucleic acids encoding the proteins CRP-1 and B7R1 are useful
PT in the treatment, prevention and diagnosis of T cell mediated disorders
PT
XX Claim 11; Fig 1A; 174pp; English.
PS
XX The present sequence represents a CRP1 (CD28 related protein-1)
CC polypeptide. The specification also describes a B7R1 (B7 related
CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
CC activation, and represent a receptor-ligand pair. CRP1 and B7R1 are
CC predicted to be a type I transmembrane protein. The nucleic acids are
CC useful for regulating T cell activation or proliferation in an animal.
CC The polypeptides are useful for treating, preventing ameliorating or
CC diagnosing a T-cell mediated disorder in an animal. They can also be
CC used to identify test molecules that bind to the polypeptides.
XX
SQ Sequence 200 AA;

Query Match 86.2%; Score 922; DB 21; Length 200;
Best Local Similarity 85.0%; Pred. No. 1.le-95;
Matches 170; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MKPYSCVFCFLIKLTGELNDLANHRMFSFHGGVQVQISCNYPETVQQLKMQLFKDR 60
Db 1 mkpyfcrvfvcflirlltgeingsadhrmfsfhngvgvqiskypetvqqlkmrfrere 60

Qy 61 VLCDLTGKSGNTVSIKPNMPCPYQLSNNSVSRFLDNADSSQGSYFLCSLIFDPPPFQ 120
Db 61 vlceltkksgnavsknplmclclhlnsnsvsflnnpdssqgsyfcslsifpppfq 120

Qy 121 EKNLSGGYLLIYESQLCCQLKWLPGVCAAFVAALLFGCIFVWFPAKKYRSVHDNPSE 180
Db 121 ernlsggylhiesqlccqlkwlpgvcaafvllfgcilliwfskkygssvhdnpse 180

Qy 181 YMFMAAVNTNKKSLAGMTS 200
Db 181 ymfmaavntnkkslagvts 200

RESULT 4
ID AAY92212 standard; Protein; 200 AA.
XX
AC AAY92212;
XX
DT 10-AUG-2000 (first entry)
XX
DE Murine Th2-specific polypeptide, m1228.
XX
KW m1288; Th2-specific; T helper cell; anti-inflammatory; antiarthritic;
KW CD28; antidiabetic; immunosuppressive; neuroprotective; dermatological;
KW antiporiatric; antiasthmatic; anti-allergic; anti-viral; ophthalmological;
KW CTLA-4; nephrotropic; anti-HIV; antibacterial.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 114..119
FT /label= conserved_ppp_motif
FT /note= "common in CD28 and CTLA-4"
FT Peptide 181..184
FT /label= YXXM_motif

/note= "common in CD28 and CTLA-4; necessary for CD28-mediated phosphatidylinositol 3-kinase activity"
WO200019988-A1.
13-APR-2000.
06-OCT-1999; 99WO-US23156.
07-OCT-1998; 98US-0168229.
26-FEB-1999; 99US-0258670.
06-OCT-1999; 99US-0413136.
XX (MILL-) MILLENNIUM PHARM INC.
XX Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J;
XX WPI; 2000-303619/26.
XX N-PSDB; AAA09054.
XX T helper (Th) 2 nucleic acids and encoded proteins, useful for the
PT diagnosis and treatment of immune and respiratory disorders such as
PT Crohn's diseases, arthritis, insulin dependent diabetes and
PT autoimmunity
XX
PS Claim 16; Page 130-131; 159pp; English.
XX
CC This Th2-specific polypeptide is encoded by a murine orthologue m1288.
CC The protein shares homology with both human and murine CD28 and CTLA-4.
CC A novel method for modulating a Th2 response, an immune response, or
CC suppressing airway inflammation or hyperresponsiveness in a mammal
CC comprises administering a Th2-specific polypeptide of the invention, an
CC antibody to such a polypeptide or allelic variants of the genes. The
CC novel DNA and polypeptide sequences are useful for treatment and
CC diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases,
CC arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis,
CC dermatitis, psoriasis, graft rejection, graft versus host diseases,
CC sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis,
CC viral infections (including human immunodeficiency virus (HIV)),
CC bacterial infections, bronchitis, cystic fibrosis, diphtheria,
CC emphysema, pneumonia, and Legionnaires disease.
XX
SQ Sequence 200 AA;

Query Match 86.2%; Score 922; DB 21; Length 200;
Best Local Similarity 85.0%; Pred. No. 1.le-95;
Matches 170; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MKPYSCVFCFLIKLTGELNDLANHRMFSFHGGVQVQISCNYPETVQQLKMQLFKDR 60
Db 1 mkpyfcrvfvcflirlltgeingsadhrmfsfhngvgvqiskypetvqqlkmrfrere 60

Qy 61 VLCDLTGKSGNTVSIKPNMPCPYQLSNNSVSRFLDNADSSQGSYFLCSLIFDPPPFQ 120
Db 61 vlceltkksgnavsknplmclclhlnsnsvsflnnpdssqgsyfcslsifpppfq 120

Qy 121 EKNLSGGYLLIYESQLCCQLKWLPGVCAAFVAALLFGCIFVWFPAKKYRSVHDNPSE 180
Db 121 ernlsggylhiesqlccqlkwlpgvcaafvllfgcilliwfskkygssvhdnpse 180

Qy 181 YMFMAAVNTNKKSLAGMTS 200
Db 181 ymfmaavntnkkslagvts 200

RESULT 5
ID AAW75958 standard; Protein; 200 AA.
XX
AC AAW75958;
XX

DT 11-DEC-1998 (first entry)
 XX Mouse cell surface protein.
 DE
 XX
 KW Mouse; cell surface protein; thymocyte; lymphocyte; cell adhesion;
 KW signal transmission; autoimmune disorder; allergy; diagnosis;
 KW mitogen-stimulated.
 XX
 XX Mus sp.
 OS
 XX WO9838216-A1.
 PN
 XX
 PD 03-SEP-1998.
 PD
 XX 27-FEB-1998; 98WO-JP00837.
 XX
 XX 26-FEB-1998; 98JP-0062217.
 XX
 PR 27-FEB-1997; 97JP-0062290.
 PR
 XX (NISR) JAPAN TOBACCO INC.
 PA
 XX Tamatani T, Tezuka K;
 XX WPI; 1998-481144/41.
 XX DR N-PSDB; AAV53200.
 XX
 XX Cell surface molecule expressed in thymocytes and lymphocytes and -
 PT mediating signal transmission and cell adhesion, and antibodies to
 PT it useful in treatment of auto-immune and allergic disorders.
 PT
 XX
 PS Claim 9; Page 110-112; 149pp; Japanese.
 XX
 CC The present sequence represents a mouse cell surface protein which is
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
 CC antibodies recognising the cell surface protein. These antibodies also
 CC produce an increase in peripheral blood lymphocytes in the presence of
 CC an antibody recognising CD3 antigen. The cell surface protein contains
 CC the amino acid sequence FPPPP in its extracellular region and the
 CC sequence YPMF in its intracellular region. The cell surface protein can
 CC be used in the prevention and treatment of autoimmune and allergic
 CC diseases, and in the diagnosis and investigation of such disorders.
 CC
 XX Sequence 200 AA;
 SQ
 Query Match 84.8%; Score 907; DB 19; Length 200;
 Best Local Similarity 84.0%; Pred. No. 5.6e-94;
 Matches 168; Conservative 14; Mismatches 18; Indels 0; Gaps 0;
 Qy 1 MKPYFSCVFVFCFLIKLTGELNDLANHRMFSFHDGGVQISCNYPETVQQLKMLFKDRE 60
 Db 1 mkpyfchvfvcfliriltgeingsadhrmfshngvgqiskypetvqqlkmlfrere 60
 Qy 61 VLCDLTTKSGNTVSTKNPMSCPYQLSNNSVSFFLNDNADSSQGSYFLCSLSIFDPPPFQ 120
 Db 61 vlceltksgnnavsiknplmcliyhsnnsvsfflnpdpssggyfcslsifdpppfq 120
 Qy 121 EKNLSGGVLLIYESQLCCOLKWLPGVCAAFVAALLFCCIFIVWFAKKYRSSVHDENSE 180
 Db 121 ernlsqgyllhyesqlccqiklwpvglpavllpavllfvcillilwfskkygssvhdnse 180
 Qy 181 YMFMAAVNTNKKSLAGTMS 200
 Db 181 ymfmaavntnkkslagtms 200
 RESULT 6
 AAW75956
 ID AAW75956 standard; Protein; 199 AA.
 XX
 AC AAW75956;
 XX

DT 11-DEC-1998 (first entry)
 XX Human cell surface protein #1.
 DE
 XX
 KW Human; cell surface protein; thymocyte; lymphocyte; cell adhesion;
 KW signal transmission; autoimmune disorder; allergy; diagnosis;
 KW mitogen-stimulated.
 XX
 XX Homo sapiens.
 OS
 XX WO9838216-A1.
 PN
 XX
 PD 03-SEP-1998.
 PD
 XX 27-FEB-1998; 98WO-JP00837.
 XX
 XX 26-FEB-1998; 98JP-0062217.
 XX
 PR 27-FEB-1997; 97JP-0062290.
 PR
 XX (NISB) JAPAN TOBACCO INC.
 PA
 XX Tamatani T, Tezuka K;
 XX WPI; 1998-481144/41.
 XX DR N-PSDB; AAV53198.
 XX
 XX Cell surface molecule expressed in thymocytes and lymphocytes and -
 PT mediating signal transmission and cell adhesion, and antibodies to
 PT it useful in treatment of auto-immune and allergic disorders.
 PT
 XX
 PS Claim 2; Page 99-101; 149pp; Japanese.
 XX
 CC The present sequence represents a human cell surface protein which is
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
 CC antibodies recognising the cell surface protein. These antibodies also
 CC produce an increase in peripheral blood lymphocytes in the presence of
 CC an antibody recognising CD3 antigen. The cell surface protein contains
 CC the amino acid sequence FPPPP in its extracellular region and the
 CC sequence YPMF in its intracellular region. The cell surface protein can
 CC be used in the prevention and treatment of autoimmune and allergic
 CC diseases, and in the diagnosis and investigation of such disorders.
 CC
 XX Sequence 199 AA;
 SQ
 Query Match 65.5%; Score 701; DB 19; Length 199;
 Best Local Similarity 67.9%; Pred. No. 9.7e-71;
 Matches 133; Conservative 17; Mismatches 42; Indels 4; Gaps 2;
 Qy 4 YFSCVFVFCFLIKLTGELNDLANHRMFSFHDGGVQISCNYPETVQQLKMLFKDREVL 63
 Db 7 yf---flfcrikvlteingsanyemfihngvgqilckypdivqgqfkmllkqgqilc 63
 Qy 64 DLTKSGNTVSTKNPMSCPYQLSNNSVSFFLNDNADSSQGSYFLCSLSIFDPPPFQBN 123
 Db 64 dltksgntvstksikfchsqslsnnsvsfflndhshanyfconlsifdpppf-kvt 122
 Qy 124 LSGGYLLIYESQLCCOLKWLPGVCAAFVAALLFCCIFIVWFAKKYRSSVHDENSEYMF 183
 Db 123 ltggyllhyesqlccqiklwpvglpavllpavllfvcillilwfskkygssvhdnseymf 182
 Qy 184 MAAVNTNKKSLAGMT 199
 Db 184 mravntakksrltdvt 198
 RESULT 7
 AAW75957
 ID AAW75957 standard; Protein; 199 AA.
 XX
 AC AAW75957;
 XX

DT 11-DEC-1998 (first entry)
DE Human cell surface protein #2.
XX
KW Human; cell surface protein; thymocyte; lymphocyte; cell adhesion;
KW signal transmission; autoimmune disorder; allergy; diagnosis;
KW mitogen-stimulated.
XX
OS Homo sapiens.
XX WO9838216-A1.
XX
XX 03-SEP-1998.
XX
XX 27-FEB-1998; 98WO-JP00837.
XX
XX 26-FEB-1998; 98JP-0062217.
XX
XX 27-FEB-1997; 97JP-0062290.
XX
XX (NISR) JAPAN TOBACCO INC.
XX
XX amatanani T, Tezuka K;
XX
XX WPI; 1998-481144/41.
XX
XX N-PSDB; AAV53199.
XX
XX Cell surface molecule expressed in thymocytes and lymphocytes and
PT mediating signal transmission and cell adhesion, and antibodies to
PT it useful in treatment of autoimmune and allergic disorders.
XX
XX
XX Claim 9; Page 101-105; 149pp; Japanese.
XX
XX The present sequence represents a human cell surface protein which is
CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
CC antibodies recognising the cell surface protein. These antibodies also
CC produce an increase in peripheral blood lymphocytes in the presence of
CC an antibody recognising CD3 antigen. The cell surface protein contains
CC the amino acid sequence FQPPPF in its extracellular region and the
CC sequence YFMW in its intracellular region. The cell surface protein can
CC be used in the prevention and treatment of autoimmune and allergic
CC diseases, and in the diagnosis and investigation of such disorders.
XX
XX Sequence 199 AA;
SQ
Query Match 65.5%; Score 701; DB 19; Length 199;
Best Local Similarity 67.9%; Pred. No. 9.7e-71;
Matches 133; Conservative 17; Mismatches 42; Indels 4; Gaps 2;
QY 4 YFSCVFVFCFLIKLTGELNDLANHRMFSFDGGVQVQISCNYPETVQQLKMQLFKDREVLC 63'
Db 7 YF--flclrikvitgeingsanyemfifngvqilckypdivqgqkmqilkggqilc 63
QY 64 DLTKTGSGNTVSIKPNMPCPYQLNSNSVSFFLDNADSSQGSYFLCSLSIFDPPPPFOEKN 123
Db 64 dlctksgntvtsiklksfchsqslsnsvsfflyndshanyfncisifdpppf-kvt 122
QY 124 LSGGYLLIYESQCCQLKLWLPVGCAAFVAALLFGCIFVWFACKKRRSSVHDNPSEYMF 183
Db 123 ltggylhiyesqlccqlkfwlpigcaafvfvvcilgcilicwtlctkkyssvhdnpgeymf 182
QY 184 MAAVNTNKKSLAGMT 199
Db 183 mravntakksrltdvt 198
RESULT 8
AY08026
ID AY08026 standard; Protein; 199 AA.
XX
XX AC AY08026;
XX

DT 08-JUL-1999 (first entry)
DE Human activated T-lymphocyte protein 8F4.
XX
XX T-lymphocyte; human; 8F4; T cell co-stimulation; activated; CD4+; CD8+;
KW anticancer; antiviral; anti-asthma; immunomodulator; proliferation;
KW T cell activation; cytokine synthesis; regulatory element; B cell;
KW T cell-dependent antibody production; treatment; prevention; cancer;
KW autoimmune disease; transplant rejection; immune system regulation;
KW disorder; acquired immune deficiency syndrome; AIDS; asthma.
XX
XX Homo sapiens.
XX
XX WO9915553-A2.
XX
XX 01-APR-1999.
XX
XX 23-SEP-1998; 98WO-DE02896.
XX
XX 11-MAY-1998; 98DE-1021060.
XX
XX 23-SEP-1997; 97DE-1041929.
XX
XX (DEKO-) DEUT KOCH INST ROBERT.
XX
XX (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
XX
XX Kroczek R;
XX
XX WPI; 1999-276975/23.
XX
XX N-PSDB; AAX37661.
XX
XX Polypeptide 8F4 co-stimulates T cells and is present only on
PT activated cells
PT
XX Claim 2; Page 24; 47pp; German.
XX
XX This invention describes a novel human protein, 8F4, and its encoding
CC nucleic acid which co-stimulates T cells and is present on activated CD4+
CC and CD8+ T cells but not on resting or activated B cells, granulocytes,
CC monocytes, natural killer or dendritic cells. 8F4 has anticancer,
CC antiviral, anti-asthma and immunomodulatory activity. 8F4 provides a
CC strong co-stimulatory signal for T cell activation, i.e. it amplifies
CC proliferation of T cells, synthesis of certain cytokines and other
CC regulatory agents, and improves T cell-dependent antibody production
CC by B cells. Agents that inhibit 8F4 are used to treat or prevent
CC autoimmune diseases, to prevent transplant rejection and to treat
CC disorders of immune system regulation. 8F4, or cells that express it,
CC is/are used to treat or prevent cancers, acquired immune deficiency
CC syndrome, asthma and chronic infectious diseases (e.g. hepatitis B or C).
XX
XX Sequence 199 AA;
SQ
Query Match 65.5%; Score 701; DB 20; Length 199;
Best Local Similarity 67.9%; Pred. No. 9.7e-71;
Matches 133; Conservative 17; Mismatches 42; Indels 4; Gaps 2;
QY 4 YFSCVFVFCFLIKLTGELNDLANHRMFSFDGGVQVQISCNYPETVQQLKMQLFKDREVLC 63
Db 7 YF--flclrikvitgeingsanyemfifngvqilckypdivqgqkmqilkggqilc 63
QY 64 DLTKTGSGNTVSIKPNMPCPYQLNSNSVSFFLDNADSSQGSYFLCSLSIFDPPPPFOEKN 123
Db 64 dlctksgntvtsiklksfchsqslsnsvsfflyndshanyfncisifdpppf-kvt 122
QY 124 LSGGYLLIYESQCCQLKLWLPVGCAAFVAALLFGCIFVWFACKKRRSSVHDNPSEYMF 183
Db 123 ltggylhiyesqlccqlkfwlpigcaafvfvvcilgcilicwtlctkkyssvhdnpgeymf 182
QY 184 MAAVNTNKKSLAGMT 199
Db 183 mravntakksrltdvt 198

CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angioinfectious disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC The present sequence represents a human secreted protein of
CC the invention.

XX
SQ Sequence 199 AA;

Query Match 65.5%; Score 701; DB 22; Length 199;
Best Local Similarity 67.9%; Pred. No. 9.7e-71;
Matches 133; Conservative 17; Mismatches 42; Indels 4; Gaps 2;

QY 4 YFSCVFVFCFLIKLTGELNDLANHRMFSFDHGGVQVSCNYPETVQQLKMLFKDREVLG 63
Db 7 YFSCVFVFCFLIKLTGELNDLANHRMFSFDHGGVQVSCNYPETVQQLKMLFKDREVLG 63
QY 64 DLTKGSGNTVSTKNMPCPYQLSNNSVSFFLNDADSSQGSYFLCSLISIFDPPPFQKN 123
Db 64 dlTKGSGNTVSTKNMPCPYQLSNNSVSFFLNDADSSQGSYFLCSLISIFDPPPFQKN 123
QY 124 LSGGYLLIYESQLCCQLKMLPVGCAAFVALLFGCIFVWFAKKYKSSVHDNPSYMF 183
Db 123 ltggyllhyesqlccqlkfwlpigcaafvvcilgclilcwttkkysvhdnpsymf 182
QY 184 MAAVNTNKKSLAGMT 199
Db 183 mravntakksrltdvt 198

RESULT 11
AAE03460
ID AAE03460 standard; Protein; 199 AA.
AC AAE03460;
XX AAE03460 (first entry)
DE Human gene 2 encoded secreted protein HT25G64, SEQ ID NO: 143.

XX Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW inflammation; neurological disorder; Alzheimer's disease; food additive;
KW angioinfectious disorder; kidney disorder; gastrointestinal disorder; allergy;
KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW cell culture; chemotaxis; vulnery; binding partner identification;
KW gene therapy.

XX Homo sapiens.
XX Key Location/Qualifiers
FH 1..19
FT Peptide /label= Signal_peptide
FT 20..199
FT Protein /note= "Mature human secreted protein"
XX W0200132675-A1.
PN

XX 10-MAY-2001.
XX 25-OCT-2000; 2000WO-US29363.
XX 29-OCT-1999; 99US-0162239.
XX 30-JUN-2000; 2000US-0215139.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Komatsoulis GA, Wei P, Baker KP, Young PE;
XX WPI; 2001-328772/34.
XX N-PSDB; AAD07842.
XX Thirty two human secreted proteins, useful for treating cancers,
XX hyperproliferative disorders, inflammatory disorders, neurological
XX disorders, autoimmune diseases and cardiovascular disorders -
XX Claim 11; Page 489-490; 576pp; English.

XX AAD07809-AAD07907 represent cDNAs corresponding to 32 human secreted
XX protein genes, and AAE03427-AAE03523 represent the proteins they encode.
XX AAE03524-AAE03537 represent human secreted protein fragments or variants.
XX The secreted proteins and their genes are useful for preventing, treating
XX or ameliorating medical conditions, e.g., by protein or gene therapy.
XX Pathological conditions can be diagnosed by determining the amount of the
XX new protein in a sample or by determining the presence of mutations in
XX the new genes. Specific uses are described for each of the 32 genes,
XX based on the tissues in which they are most highly expressed, and include
XX developing products for the diagnosis or treatment of proliferative
XX disorders, cancer, tumours, foetal and developmental abnormalities,
XX haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
XX diseases (e.g., rheumatoid arthritis), inflammation, allergies,
XX neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
XX cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
XX psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
XX angioinfectious disorders, kidney disorders, gastrointestinal disorders,
XX pregnancy related disorders, endocrine disorders, and infections. The
XX proteins can also be used to aid wound healing and epithelial cell
XX proliferation, to prevent skin aging due to sunburn, to maintain organs
XX before transplantation, for supporting cell culture of primary tissues,
XX to regenerate tissues, to identify their cognate ligands or binding
XX partners, and in chemotaxis, and can be used as a food additive or
XX preservative to modify storage properties. Antibodies specific for a
XX protein of the invention can be used in alleviating symptoms associated
XX with the disorders mentioned above, and in diagnostic immunoassays e.g.,
XX radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
XX The present sequence represents a human secreted protein of
XX the invention.

XX Sequence 199 AA;

Query Match 65.5%; Score 701; DB 22; Length 199;
Best Local Similarity 67.9%; Pred. No. 9.7e-71;
Matches 133; Conservative 17; Mismatches 42; Indels 4; Gaps 2;

QY 4 YFSCVFVFCFLIKLTGELNDLANHRMFSFDHGGVQVSCNYPETVQQLKMLFKDREVLG 63
Db 7 YFSCVFVFCFLIKLTGELNDLANHRMFSFDHGGVQVSCNYPETVQQLKMLFKDREVLG 63
QY 64 DLTKGSGNTVSTKNMPCPYQLSNNSVSFFLNDADSSQGSYFLCSLISIFDPPPFQKN 123
Db 64 dlTKGSGNTVSTKNMPCPYQLSNNSVSFFLNDADSSQGSYFLCSLISIFDPPPFQKN 123
QY 124 LSGGYLLIYESQLCCQLKMLPVGCAAFVALLFGCIFVWFAKKYKSSVHDNPSYMF 183
Db 123 ltggyllhyesqlccqlkfwlpigcaafvvcilgclilcwttkkysvhdnpsymf 182
QY 184 MAAVNTNKKSLAGMT 199
Db 183 mravntakksrltdvt 198

PT Crohn's diseases, arthritis, insulin dependent diabetes and
XX autoimmunity

PS Claim 16; Page 138-139; 159pp; English.

XX This Th2-specific polypeptide, which has similarity to human CD28 and
CC human CTLA-4 is encoded by human orthologue h1228.
CC A novel method for modulating a Th2 response, an immune response, or
CC suppressing airway inflammation or hyperresponsiveness in a mammal
CC comprises administering a Th2-specific polypeptide of the invention, an
CC antibody to such a polypeptide or allelic variants of the genes. The
CC novel DNA and polypeptide sequences are useful for treatment and
CC diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases,
CC arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis,
CC dermatitis, psoriasis, graft rejection, graft versus host diseases,
CC sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis,
CC viral infections (including human immunodeficiency virus (HIV)),
CC bacterial infections, bronchitis, cystic fibrosis, diptheria,
CC emphysema, pneumonia, and Legionnaires disease.

XX Sequence 198 AA;

Query Match 64.1%; Score 685.5; DB 21; Length 198;
Best Local Similarity 67.3%; Pred. No. 5.4e-69;
Matches 132; Conservative 17; Mismatches 42; Indels 5; Gaps 3;
QY 4 YFSCVFVFCFLIKLTGEINDLIANHRMFSFHDGGVQVQISCNYPETVQQLKMQLFKDEVLIC 63
DB 7 YF---fLcLrikvltgeinsanyemfifngvgqilckypdivgqfkmqlkggqilc 63
QY 64 DITKTKGSGNTVSIKPNMPCPYQLSNNSVSFFLDNADSSQGSYFLCSLSIFDPPPFQEK 123
DB 64 dltktksgntvsklksfchsqslsnsvsfflyldhshanyfcnlisifdpppf-kvt 122
QY 124 LSGGYLLIYESOLCCQLKWLVPVGAFAALLFGCIFTWFAKKYRSSVHDNPSEYMF 183
DB 123 lcggylhyesqlccqlkfwlpigcaafvvcilgcilicwlt-kkyssvhdnpgeymf 181
QY 184 MAAVNTNKKSLAGMT 199
DB 182 mravntakksrltdvt 197

RESULT 14
AAB67717
ID AAB67717 standard; Protein; 380 AA.

XX AAB67717;

DT 11-JUN-2001 (first entry)

DE Amino acid sequence of mICOS-mIgG2m fusion protein.

XX GL50; antigen; antigen presenting cell; T cell proliferation; tumour;
KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
KW acquired immune deficiency syndrome; AIDS; vaccine.

OS Synthetic.

OS Mus musculus.

XX WO200121796-A2.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US25892.

XX 21-SEP-1999; 99US-0155043.

XX (GEMY) GENETICS INST INC.

XX Ling V, Dunussi-Joannopolulos K;

XX

WPI: 2001-244938/25.
N-PSDB; AAF79940.

DR New isolated nucleic acid encoding a GL50 polypeptide for modulating a
XX immune response and reducing the proliferation of a tumour cell -
PT Immune response; Fig 27B; 195pp; English.
PS Disclosure; Fig 27B; 195pp; English.

XX The present sequence represents a fusion protein, comprising murine ICOS
CC (mICOS) and murine IgG2a (mIgG2A). The fusion protein is used in the
CC course of the invention. The specification describes GL50 polypeptides.
CC GL50 molecules are antigens on the surface of antigen presenting cells,
CC which costimulate T cell proliferation and bind to costimulatory receptor
CC ligands on T cells. GL50 modulating agents are used to modulate an immune
CC response in a subject. GL50 polypeptides are used to modulate T cell
CC costimulation, and to reduce the proliferation of a tumour cell. Diseases
CC that can be treated using GL50 molecules are graft-versus-host disease,
CC autoimmune disease, allergies, acquired immune deficiency syndrome
CC (AIDS), and viral infections. The GL50 molecules can be used in vaccines.
CC GL50 polynucleotides can be used to locate gene regions associated with
CC genetic disease, in tissue typing, and in forensic identification of a
CC biological sample.

XX Sequence 380 AA;

Query Match 51.6%; Score 552; DB 22; Length 380;
Best Local Similarity 83.6%; Pred. No. 1.6e-53;
Matches 102; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 21 ELNDLIANHRMFSFHDGGVQVQISCNYPETVQQLKMQLFKDEVLCDLTKGSGNTVSIKPN 80

DB 26 eingsadhrmfsfhgvgvqiscypetvqqlkmrlfrerevceltktkgsgnavsiknp 85

QY 81 MSCPTQLSNNSVSFFLDNADSSQGSYFLCSLSIFDPPPFQERNLSGGYLLIYESQLCCOL 140

DB 86 mclcyhlslsnsvsfflnpdssgsgyyfcslsifdpppfqernlsggyhlhyesqlccql 145

QY 141 KL 142

DB 146 kl 147

RESULT 15

AAB67716

ID AAB67716 standard; Protein; 379 AA.

XX AAB67716;

DT 11-JUN-2001 (first entry)

DE Amino acid sequence of hICOS-mIgG2m fusion protein.

XX GL50; antigen; antigen presenting cell; T cell proliferation; tumour;
KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
KW acquired immune deficiency syndrome; AIDS; vaccine.

OS Synthetic.

OS Homo sapiens.

OS Mus musculus.

XX WO200121796-A2.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US25892.

XX 21-SEP-1999; 99US-0155043.

XX (GEMY) GENETICS INST INC.

XX Ling V, Dunussi-Joannopolulos K;

XX

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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:27:00 ; Search time 28.8 Seconds
(without alignments)
169.622 Million cell updates/sec

Title: US-09-383-551B-13

Perfect score: 1070

Sequence: 1 MKPYSCVFVFCFLIKLLTG.....YMFMAVNTKSLAGMTS 200

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

To: Number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	13.1	220	3	US-08-228-208A-21
2	130.5	12.2	223	1	Sequence 21, Appli
3	130.5	12.2	223	1	Sequence 5, Appli
4	130.5	12.2	223	2	US-08-459-818-25
5	130.5	12.2	223	2	Sequence 25, Appli
6	130.5	12.2	223	2	US-08-889-666-25
7	130.5	12.2	223	2	Sequence 25, Appli
8	130.5	12.2	223	2	US-08-465-078-25
9	130.5	12.2	223	2	Sequence 25, Appli
10	130.5	12.2	223	2	US-08-725-776-25
11	130.5	12.2	223	2	Sequence 25, Appli
12	130.5	12.2	223	2	US-08-488-062-25
13	130.5	12.2	223	2	Sequence 25, Appli
14	130.5	11.3	218	3	US-08-228-208A-20
15	116.5	10.9	134	3	US-08-630-172-3
16	116.5	10.9	134	4	US-09-375-419-3
17	116.5	10.9	134	4	US-09-375-419-3
18	112.5	10.5	367	3	US-08-630-172-19
19	112.5	10.5	367	3	US-09-375-419-19
20	110.5	10.3	110	4	US-08-460-384-33
21	108.5	10.1	225	1	US-08-505-058-4
22	108.5	10.1	225	2	US-08-459-818-24
23	108.5	10.1	225	2	US-08-889-666-24
24	108.5	10.1	225	2	US-08-465-078-24
25	108.5	10.1	225	2	US-08-488-062-24
26	108.5	10.1	225	2	US-08-725-776-24
27	108.5	10.1	225	2	US-08-488-062-24
28	97	9.1	218	3	US-08-228-208A-19
29	90.5	8.5	221	3	US-08-228-208A-22
30	86	8.0	225	1	US-08-505-058-3
31	86	8.0	225	2	US-08-459-818-23
32	86	8.0	225	2	US-08-889-666-23
33	86	8.0	225	2	US-08-465-078-23
34	86	8.0	225	2	US-08-725-776-23
35	86	8.0	225	2	US-08-488-062-23

28 81.5 7.6 117 2 US-08-529-878B-39 Sequence 39, Appli
29 81.5 7.6 226 1 US-08-505-058-6 Sequence 6, Appli
30 81.5 7.6 226 2 US-08-459-818-26 Sequence 26, Appli
31 81.5 7.6 226 2 US-08-889-666-26 Sequence 26, Appli
32 81.5 7.6 226 2 US-08-465-078-26 Sequence 26, Appli
33 81.5 7.6 226 2 US-08-725-776-26 Sequence 26, Appli
34 81.5 7.6 226 2 US-08-488-062-26 Sequence 26, Appli
35 76 7.1 803 1 US-08-158-232-10 Sequence 10, Appli
36 76 7.1 803 1 US-08-304-626-10 Sequence 10, Appli
37 76 7.1 803 1 US-08-316-301A-12 Sequence 10, Appli
38 76 7.1 803 2 US-08-611-928-10 Sequence 10, Appli
39 76 7.1 803 3 US-09-173-891-10 Sequence 10, Appli
40 76 7.1 803 4 US-09-076-137-12 Sequence 12, Appli
41 76 7.1 803 5 PCT-US92-0362A-12 Sequence 12, Appli
42 75 7.0 682 2 US-08-436-900A-4 Sequence 4, Appli
43 74.5 7.0 223 3 US-08-228-208A-17 Sequence 17, Appli
44 73.5 6.9 474 4 US-09-362-473-4 Sequence 4, Appli
45 73 6.8 187 1 US-08-067-684-14 Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-08-228-208A-21
; Sequence 21, Application US/08228208A
; Patent No. 6090914
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Wallace, Philip M.
; TITLE OF INVENTION: CTAA4/CD28Ig HYBRID FUSION
; TITLE OF INVENTION: PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,208A
; FILING DATE: 15-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-30US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310 445-1140
; TELEFAX: 310 445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-228-208A-21

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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:27:45 ; Search time 37.55 Seconds
(without alignments)
511.794 Million cell updates/sec

Title: US-09-383-551b-13
Perfect score: 1070
Sequence: 1 MKPYFSCVFVFCFLIKLLTG.....YMFMAAVNTNKKSLRAGMTS 200

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

To: number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

- Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1070	100.0	200	2 JC7397	activation-inducib
2	1056	98.7	216	2 JC7396	activation-inducib
3	701	65.5	199	2 S78340	inducible T-cell c
4	141	13.2	220	1 RWH028	T-cell surface gly
	131	12.2	221	2 I46689	CD28 precursor - r
	108.5	10.1	218	2 S24413	T-cell surface gly
	104	9.7	173	2 I46197	cell surface prote
8	99	9.3	218	2 A43523	T-cell surface gly
9	92.5	8.6	221	2 S25168	CHR28 protein - ch
10	84.5	7.9	402	2 S58477	rdsl protein - fis
11	80.5	7.5	360	2 T26270	hypothetical prote
12	79.5	7.4	658	2 T39495	hypothetical prote
13	79	7.4	383	2 T21946	hypothetical prote
14	78	7.3	488	2 A42491	NADH dehydrogenase
15	77.5	7.2	964	2 E71460	probable outer mem
16	77.5	7.2	1036	2 S55984	probable membrane
17	77	7.2	817	2 T25758	hypothetical prote
18	76.5	7.1	1475	2 T29809	hypothetical prote
19	75.5	7.1	694	2 T33561	hypothetical prote
20	75.5	7.1	1351	2 C71607	hypothetical prote
21	75	7.0	186	2 S08614	cytotoxic T-lympho
22	75	7.0	223	2 T09536	cytotoxic T-lympho
23	75	7.0	681	2 S27868	givr-1 protein - m
24	74.5	7.0	1289	2 F72308	hypothetical prote
25	74	6.9	597	1 S53711	C4BP alpha chain p
26	74	6.9	2120	2 T30243	alpha tectorin - c
27	73.5	6.9	346	1 S03347	retinal degenerati
28	73.5	6.9	426	2 T41682	hypothetical prote
29	73	6.8	274	2 A54419	neutrophil inhibit

30	73	6.8	277	2 AH1710	maltodextrase util
31	73	6.8	787	2 H90543	conserved hypothet
32	72.5	6.8	489	2 S25943	NADH dehydrogenase
33	72.5	6.8	572	2 B28474	phosphotransferase
34	72.5	6.8	636	2 T06793	receptor kinase ho
35	72	6.7	260	2 T28119	hypothetical prote
36	72	6.7	647	2 D95098	topoisomerase IV,
37	72	6.7	758	2 C96749	hypothetical prote
38	72	6.7	1296	2 I40645	botulinum neurotox
39	72	6.7	1317	2 A54831	nuclear pore compl
40	71.5	6.7	184	2 A81280	probable integral
41	71.5	6.7	426	2 T51861	hypothetical prote
42	71.5	6.7	454	2 JC4886	bleomycin hydrolas
43	71.5	6.7	679	2 I52822	leukemia virus rec
44	71.5	6.7	1290	2 S73653	DNA-directed RNA p
45	71.5	6.7	1337	2 B64993	hypothetical prote

ALIGNMENTS

RESULT 1

JC7397

activation-inducible lymphocyte immuno-mediatory molecule-2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000

C:Accession: JC7397; PC7100

R:Tezuka, K.; Tsuji, T.; Hirano, D.; Tamatani, T.; Sakamaki, K.; Kobayashi, Y.; Kamad Biochem. Biophys. Res. Commun. 276, 335-345, 2000

A:Title: Identification and characterization of rat AILIM/ICOS, a novel T-cell costim

A:Reference number: JC7396

A:Contents: Spleen

A:Accession: JC7397

A:Molecule type: mRNA

A:Residues: 1-200 <TEZ>

A:Cross-references: DDBJ:AB023134

A:Accession: PC7100

A:Molecule type: protein

A:Residues: 21-40 <TE2>

C:Comment: This protein is an inducible cell surface glycoprotein, and a type I trans on, and plays an important role for the maturation or selection of T cells in thymus.

C:Genetics:

A:Gene: ailim-2

C:Keywords: glycoprotein; T-cell; transmembrane protein

Query Match 100.0%; Score 1070; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2e-94;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKPYFSCVFVFCFLIKLLTGELNDLANHRMFSFHDGGVQISCNYPETVQOLKMLFKDRE 60

Db 1 MKPYFSCVFVFCFLIKLLTGELNDLANHRMFSFHDGGVQISCNYPETVQOLKMLFKDRE 60

Qy 61 VLCDLTTRKSGNTVSIKNPMSCPYQLSNNSVSFLDNDSSQGSYFLCSLSIFDPPPFQ 120

Db 61 VLCDLTTRKSGNTVSIKNPMSCPYQLSNNSVSFLDNDSSQGSYFLCSLSIFDPPPFQ 120

Qy 121 EKNLSGGVLLIYESOLCCQLKMLPVGCAAFVAALLFGCIFVWFPAKKKKYRSSVHDNPSE 180

Db 121 EKNLSGGVLLIYESOLCCQLKMLPVGCAAFVAALLFGCIFVWFPAKKKKYRSSVHDNPSE 180

Qy 181 YMFMAAVNTNKKSLRAGMTS 200

Db 181 YMFMAAVNTNKKSLRAGMTS 200

RESULT 2

JC7396

activation-inducible lymphocyte immuno-mediatory molecule-1 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000

C:Accession: JC7396; PC7099

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F:165-199/Domain: Intracellular #status predicted <INT>
F:23,89,110/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          65.5%; Score 701; DB 2; Length 199;
Best Local Similarity 67.9%; Pred. NO. 2.6e-59;
Matches 133; Conservative 17; Mismatches 42; Indels 4; Gaps 2;
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[illegible]

```

D0      123  LTGGI LRIIIESQCCQJKNF WFLPGCAAF VVVC LDCGLICWLTKKATSSSVHDPNGEIMF 104
Qy      184  MAAVNTNKKSRLAGMT 199
         | | | | | | | | : |
Db      183  MRAVNTAKKSRLLTDMT 198

```

DD	103	MRAVNIARSKIDVI	1986
RESULT	4		

KWHUZR
 T-cell surface glycoprotein CD28 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999

C;Accession: A39883; A45895
R;Aruffo, A.; Seed, B.
PROC. NATL. ACAD. SCI. U.S.A. 84, 8573-8577, 1987
A;Title: Molecular cloning of a CD28 cDNA by a high-efficiency COS cell expression system

A:Reference number: A39983; MUID:88068631
A:Accession: A39983
A:Molecule type: mRNA
A:Residues: 1-220 <ARU>

A: Title: The genomic organization of the CD28 gene. Implications for the regulation of
J. Immunol. 145, 344-352, 1990
R: Lee, K.P.; Taylor, C.; Petryniak, B.; Turka, L.A.; June, C.H.; Thompson, C.B.
A: Cross-references: GB:J02988; NID:9338444; PIDN:AAA60581.1; PID:9338445
R: Lee, K.P.; Taylor, C.; Petryniak, B.; Turka, L.A.; June, C.H.; Thompson, C.B.

A:Reference number: A45895; MUID:90293482
A:Accession: A45895
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 35-134 <JEE>
A:Cross-references: GB:M37813
C:Genetics:
A:Gene: GDB:CD28

A: Cross-references: GDB:118765; OMIM:186760
A: Map position: 2q33-2q34
C: Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C: Keywords: glycoprotein; homodimer; T-cell; transmembrane protein

F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-220/Product: T-cell surface glycoprotein CD28 #status predicted <MAT>
F:19-152/Domain: extracellular #status predicted <EXT>
F:33-114/Domain: immunoglobulin domain #status predicted <IMM>

```

F:153-179/Domain: transmembrane #status predicted <TMM>
F:180-220/Domain: intracellular #status predicted <INT>
F:71.92.105.129/Binding site: carbohydrate (Asn) #status predicted

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Query Match	13.2%	Score 141;	DB 1;	Length 220;
Best Local Similarity	24.1%;	Pred No.	5.7e-06;	
1. CAC	24.1%;	24.1%	24.1%	24.1%
2. CAC	24.1%	24.1%	24.1%	24.1%
3. CAC	24.1%	24.1%	24.1%	24.1%
4. CAC	24.1%	24.1%	24.1%	24.1%
5. CAC	24.1%	24.1%	24.1%	24.1%
6. CAC	24.1%	24.1%	24.1%	24.1%
7. CAC	24.1%	24.1%	24.1%	24.1%
8. CAC	24.1%	24.1%	24.1%	24.1%
9. CAC	24.1%	24.1%	24.1%	24.1%
10. CAC	24.1%	24.1%	24.1%	24.1%
11. CAC	24.1%	24.1%	24.1%	24.1%
12. CAC	24.1%	24.1%	24.1%	24.1%
13. CAC	24.1%	24.1%	24.1%	24.1%
14. CAC	24.1%	24.1%	24.1%	24.1%
15. CAC	24.1%	24.1%	24.1%	24.1%
16. CAC	24.1%	24.1%	24.1%	24.1%
17. CAC	24.1%	24.1%	24.1%	24.1%
18. CAC	24.1%	24.1%	24.1%	24.1%
19. CAC	24.1%	24.1%	24.1%	24.1%
20. CAC	24.1%	24.1%	24.1%	24.1%

QY 30 MFSEHGGVQISCNYPETV--QQLKMQLPKDFREVLCDLTKTKGSGN--TVSIKNPMSCP 84

QY 85 YOLSNNSVFELDNADSSQGSFYLCSLSTFDPPFQEKNNLSGGYLLIYESOLCQOLK-- 142

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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:33:24 ; Search time 20.28 Seconds
(without alignments)
381.850 Million cell updates/sec

Title: US-09-383-551B-13

Perfect score: 1070

Sequence: 1 MKPYFCVFCEFLIKLLTG.....YMFMAAVNTNKKSLAGMTS 200

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

TC: number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	13.2	220	1	CD28_HUMAN
2	131	12.2	221	1	CD28_RABIT
3	129.5	12.1	219	1	CD28_BOVIN
4	115.5	10.8	218	1	CD28_RAT
5	99	9.3	218	1	CD28_MOUSE
6	92.5	8.6	221	1	CD28_CHICK
7	84.5	7.9	402	1	RDS1_SCHPO
8	77.5	7.2	964	1	PMPE_CHLTR
9	77.5	7.2	1036	1	YG35_YEAST
10	77	7.2	488	1	NU2M_OENBE
11	76	7.1	803	1	CDAA_BACTU
12	75	7.0	223	1	CTL4_HUMAN
13	73.5	6.9	346	1	RDS_MOUSE
14	72.5	6.8	489	1	NU2M_MARPO
15	72.5	6.8	572	1	PTLB_STAAR
16	72	6.7	259	1	PSA3_CAEEL
17	72	6.7	647	1	PARE_STREN
18	72	6.7	1295	1	BXA2_CLOBO
19	72	6.7	1317	1	N145_YEAST
20	71.5	6.7	454	1	BLMH_RAT
21	71.5	6.7	1290	1	RPOC_MYCPN
22	71	6.6	260	1	PCNA_DROME
23	71	6.6	345	1	RDS_BOVIN
24	71	6.6	1277	1	NPC1_PIG
25	71	6.6	1419	1	MDR_PLAFF
26	70.5	6.6	198	1	MCRS_METTM
27	70.5	6.6	354	1	RDS_CHICK
28	70.5	6.6	563	1	SVR_CHLTR
29	70.5	6.6	896	1	IF2_CHLMU
30	70	6.5	223	1	CTL4_RABIT
31	70	6.5	343	1	SLAM_MOUSE
32	70	6.5	495	1	SPKF_SYNY3
33	70	6.5	1295	1	BXA1_CLOBO

34 70 6.5 2146 1 INSR_DROME P09208 drosophila
35 70 6.5 2516 1 CCAD_DROME Q24270 drosophila
36 69.5 346 1 RDS_CANFA P52204 canis faml
37 69.5 723 1 YETA_SCHPO O14162 schizosacch
38 69.5 6.5 1092 1 DHE2_YEAST P33327 saccharomyc
39 69 6.4 396 1 CSA_HUMAN O13216 homo sapien
40 69 6.4 1237 1 YG2L_YEAST P53254 saccharomyc
41 68.5 6.4 526 1 YHVL_YEAST P38849 saccharomyc
42 68.5 6.4 544 1 DSK1_SCHPO P38616 schizosacch
43 68.5 6.4 560 1 P2B2_DROME Q27889 drosophila
44 68.5 6.4 612 1 GIDA_MYCGE P47619 mycoplasma
45 68.5 6.4 856 1 NCKX_DROME Q9u6a0 drosophila

ALIGNMENTS

RESULT 1
CD28_HUMAN
ID CD28_HUMAN STANDARD; PRT; 220 AA.
AC P10747;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T-cell-specific surface glycoprotein CD28 precursor (TP44).
GN CD28.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88068631; PubMed=2825196;
RA Aruffo A., Seed B.;
RT "Molecular cloning of a CD28 cDNA by a high-efficiency COS cell
expression system";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8573-8577(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90293482; PubMed=2162892;
RA Lee K.P., Taylor C., Petryniak B., Turka L.A., June C.H.,
Thompson C.B.;
RT "The genomic organization of the CD28 gene. Implications for the
regulation of CD28 mRNA expression and heterogeneity";
RL J. Immunol. 145:344-352(1990)
CC -!- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
AND B7-2 (B70).
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD28 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd28.htm".

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; J02988; AAA60581.1; -;
EMBL; M37815; AAA51944.1; -;
EMBL; M37812; AAA51944.1; JOINED.
EMBL; M37813; AAA51944.1; JOINED.
EMBL; M37814; AAA51944.1; JOINED.
PIR; A39983; RWHU28.
HSP; P16410; 1AHL.
MIM; 186760; -;
InterPro; IPR003600; Ig_like.
SMART; SM00410; IG_like; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.

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FT SIGNAL 1 18
FT CHAIN 19 220
FT T-CELL-SPECIFIC SURFACE GLYCOPROTEIN
FT CD28.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 152
FT DOMAIN 153 179
FT DOMAIN 180 220
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE V-TYPE DOMAIN.
FT CARBOHYD 37 137
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 38 137
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 71 71
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 92 92
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 105 105
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129
FT N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 220 AA; 25066 MW; 1D9B6552A5878D0F CRC64;

Query Match 13.2%; Score 141; DB 1; Length 220;
Best Local Similarity 24.1%; Pred. No. 1.5e-06;
Matches 41; Conservative 34; Mismatches 77; Indels 18; Gaps 5;

30 MFSFHDGGVQISCNYPETV--OOLKMQLFKDRVCLDLTKTKGSGN--TVSIKNPMSCP 84
28 MLVAVDNAVNLCKYSYNLFSREFRSLHKLGLDSAVEVCVYGVNYSQQLQVYSKGTGFNCD 87
85 YOLSNNSVSFFLDNADSSQGSYFLCSLSTFDPFPQEKNLGGYLLIYESQLCCQLKL-- 142
88 GKLGNESTVFYQLNLYVNTDIYFCKIEVMYPPYLDNEKSNGTIIHVKGKHLCPSPLPF 147
143 -----WLPVGCAAFVA--ALLFGCIFVWFAKKYRSSHVDHPNSEYMF 184
148 GPSKPFVLVVGVLACYSLVTVAFIFWVRSRSLH---SDYMMN 194

RESULT 2
CD28_RABIT STANDARD; PRT; 221 AA.
AC P42069;
DT 01-NOV-1995 (Rel. 32; Created)
DT 01-NOV-1995 (Rel. 32; Last sequence update)
DT 01-MAR-2002 (Rel. 41; Last annotation update)
DE T-cell-specific surface glycoprotein CD28 precursor.
GN CD28.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID:9986;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-B/J X CHBB:HM;
RA MEDLINE:95369849; PubMed:7642234;
RT Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
RT costimulatory molecules";
RL Immunogenetics 42:217-220(1995).
CC -!- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
CC AND B7-2 (B70). (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D49841; BAA08641.1; -.
CC InterPro: IPR003600; Ig_like.
CC SMART: SM00410; Ig_like; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 19
FT BY SIMILARITY.
```

```
FT CHAIN 20 221
FT T-CELL-SPECIFIC SURFACE GLYCOPROTEIN
FT CD28.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 151 177
FT DOMAIN 178 221
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE V-TYPE DOMAIN.
FT CARBOHYD 38 138
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 93 93
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 106 106
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 130 130
FT N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 221 AA; 25307 MW; 3DF652C9CF14F13 CRC64;

Query Match 12.2%; Score 131; DB 1; Length 221;
Best Local Similarity 22.2%; Pred. No. 1.4e-05;
Matches 39; Conservative 32; Mismatches 75; Indels 30; Gaps 6;

30 MFSFHDGGVQISCNYPETV--OOLKMQLFKDRVCLDLTKTKGSGNTVSIKNP----- 80
29 MLVAVNNEVNLCKTYNLFSEFRASLYKGADSAVEVCVVG--NFSHPHQFHTT 83
81 -MSCPYQLSNNSVSFFLDNADSSQGSYFLCSLSTFDPFPQEKNLGGYLLIYESQLCC- 138
84 GFNCCKLGNETVYLNLYVNTDIYFCKIEVMYPPYLDNEKSNGTIIHVKEQHFPC 143
139 -----QLKLWLPV---GCAAFVAALLFGCIFVWFAKKYRSSHVDHPNSEYMF 184
144 AHPSPKSTLFWLVVVGAVLAFYSMLVTVALFSCWMSKKNRLL----QSYMMN 195

RESULT 3
CD28_BOVIN STANDARD; PRT; 219 AA.
AC Q28071;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 01-MAR-2002 (Rel. 41; Last annotation update)
DE T-cell-specific surface glycoprotein CD28 precursor.
GN CD28.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE:96186531; PubMed:8606060;
RA Parsons K.R., Young J.R., Collins R.A., Howard C.J.;
RA "Cattle CTLA-4, CD28 and chicken CD28 bind CD86: MYPPPY is not
RT conserved in cattle CD28.";
RL Immunogenetics 43:388-391(1996).
CC -!- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
CC AND B7-2 (B70).
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X93304; CAA63707.1; -.
CC InterPro: IPR003600; Ig_like.
CC SMART: SM00410; Ig_like; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 18
FT T-CELL-SPECIFIC SURFACE GLYCOPROTEIN
FT CHAIN 19 219
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:34:34 ; Search time 63.42 Seconds
(without alignments)
545.553 Million cell updates/sec

Title: US-09-383-551B-13
Perfect score: 1070
Sequence: 1 MKPYFSCVFVFCFLIKLLTG.....YMFMAAVNTNKKSLACMTS 200

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 562222 seqs, 172994929 residues

Tr number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rviro:
16: sp_bacteriaph:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	1070	100.0	200	11 Q9RLT7	Q9RLT7 rattus norv
2	1056	98.7	216	11 Q9WVR9	Q9WVR9 rattus norv
3	922	86.2	200	11 Q9WVS0	Q9WVS0 mus musculu
4	922	86.2	200	11 Q9JL17	Q9JL17 mus musculu
5	701	65.5	199	4 Q9Y6W8	Q9Y6W8 homo sapien
6	137	12.8	220	6 Q9BDM8	Q9BDM8 macaca neme
7	131.5	12.3	219	6 Q97630	Q97630 oviss aries
8	131	12.2	220	6 Q9BDM6	Q9BDM6 macaca mula
9	130	12.1	220	6 Q9BDN5	Q9BDN5 cercocebus
10	123	11.5	220	6 Q9BDN8	Q9BDN8 papio anubi
11	117	10.9	221	6 Q9N2I4	Q9N2I4 felis silve
12	116	10.8	221	6 Q9N0N8	Q9N0N8 canis fami
13	110.5	10.3	221	6 Q9BDN2	Q9BDN2 callithrix
14	110	10.3	220	6 Q9GKP3	Q9GKP3 canis fami
15	108	10.1	221	6 Q9GKP3	Q9GKP3 canis fami
16	104	9.7	173	6 Q28289	Q28289 canis fami

17	100	9.3	221	11 Q9JLV4	Q9JLV4 marmota mon
18	88.5	8.3	223	6 Q9BDP1	Q9BDP1 aotus trivi
19	87	8.1	579	10 Q9MAG9	Q9MAG9 arabidopsi
20	87	8.1	3027	4 Q9Y4B5	Q9Y4B5 homo sapien
21	83	7.8	401	4 Q96NFO	Q96NFO homo sapien
22	82	7.7	223	11 Q9JLV3	Q9JLV3 marmota mon
23	82	7.7	228	4 Q9H1E0	Q9H1E0 homo sapien
24	82	7.7	503	4 Q9NVP4	Q9NVP4 homo sapien
25	81	7.6	223	6 Q9BDC4	Q9BDC4 macaca mula
26	81	7.6	223	6 Q9BDN7	Q9BDN7 papio anubi
27	81	7.6	1531	4 Q96L95	Q96L95 homo sapien
28	80.5	7.5	360	5 Q9XUJ9	Q9XUJ9 caenorhabdi
29	80	7.5	857	10 Q9LO97	Q9LO97 arabidopsi
30	79.5	7.4	658	3 Q94731	Q94731 schizosacch
31	79	7.4	485	5 Q20139	Q20139 caenorhabdi
32	77.5	7.2	332	13 Q9IB08	Q9IB08 spherooides
33	77.5	7.2	927	5 Q94232	Q94232 caenorhabdi
34	77.5	7.2	2919	12 Q85431	Q85431 rice stripe
35	76.5	7.1	1432	5 Q18647	Q18647 caenorhabdi
36	76	7.1	139	1 Q9UXE6	Q9UXE6 sulfolobus
37	76	7.1	682	11 Q9QVW6	Q9QVW6 mus musculu
38	75.5	7.1	337	5 Q9TZD7	Q9TZD7 caenorhabdi
39	75.5	7.1	417	8 Q9G341	Q9G341 leucobryum
40	75.5	7.1	650	5 Q9W1C7	Q9W1C7 drosophila
41	75.5	7.1	1212	13 Q42347	Q42347 gallus gall
42	75.5	7.1	1351	5 Q96242	Q96242 plasmodium
43	75	7.0	681	11 Q61609	Q61609 mus musculu
44	75	7.0	681	11 Q91Y09	Q91Y09 mus musculu
45	74.5	7.0	417	8 Q9G3A1	Q9G3A1 ceratodon p

ALIGNMENTS

RESULT 1

Q9RLT7 PRELIMINARY; PRT; 200 AA.
AC Q9RLT7;
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
DE PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20462959; PubMed=11006126;
RA Tezuka K., Tsuji T., Hirano D., Tamatani T., Sakamaki K.,
RA Kobayashi Y., Kamada M.;
RT "Identification and characterization of rat AILIM/ICOS, a novel T-cell
stimulatory molecule, related to the CD28/CTLA4 family.";
RL Biochem. Biophys. Res. Commun. 276:335-345(2000).
DR EMBL; AB023134; BAA82128.1; -.
KW Signal.
FT SIGNAL
SQ SEQUENCE 200 AA; 22529 MW; 0A74C35581F129D4 CRC64;

Query Match 100.0%; Score 1070; DB 11; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.4e-106;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPYFSCVFVFCFLIKLLTGELNDLANHRMFSFHGGVVOISCNYPETVQOLKMOFKDRE 60
|||||

Db 1 MKPYFSCVFVFCFLIKLLTGELNDLANHRMFSFHGGVVOISCNYPETVQOLKMOFKDRE 60
|||||

QY 61 VLCDLTKTGSGNTVSIKNPMSCPYQLSNNSVSFFLDNADSSQGSYFLCSLIFDPPFPFQ 120
|||||

Db 61 VLCDLTKTGSGNTVSIKNPMSCPYQLSNNSVSFFLDNADSSQGSYFLCSLIFDPPFPFQ 120
|||||

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QY 121 EKNLSGGYLLIYESQLCCQLKWLPGCAAFVAALLFGCIFTWFAKKYRSVHDPNSE 180
Db 121 EKNLSGGYLLIYESQLCCQLKWLPGCAAFVAALLFGCIFTWFAKKYRSVHDPNSE 180

QY 181 YMFMAAVNTNKKSLAGMTS 200
Db 181 YMFMAAVNTNKKSLAGMTS 200

RESULT 2
Q9WVR9 PRELIMINARY; PRT; 216 AA.
ID Q9WVR9;
AC Q9WVR9;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
DE PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RX MEDLINE=20462959; PubMed=11006126;
RA Tezuka K., Tsuji T., Hirano D., Tamatani T., Sakamaki K.,
RA Kobayashi Y., Kanada M.;
RT "Identification and characterization of rat AILIM/ICOS, a novel T-cell
RT costimulatory molecule, related to the CD28/CTLA4 family.";
RL Biochem. Biophys. Res. Commun. 276:335-345(2000).
DR EMBL; AB023133; BAA82127.1; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 216 AA; 24260 MW; 772E01320982B15A CRC64;

Query Match 98.7%; Score 1056; DB 11; Length 216;
Best Local Similarity 100.0%; Pred. No. 4.8e-105;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPYFCVFCFLIKLTGELNDLANHRMFSFHGGVQVSCNYPETVQOLKMLFKDRE 60
Db 1 MKPYFCVFCFLIKLTGELNDLANHRMFSFHGGVQVSCNYPETVQOLKMLFKDRE 60

QY 61 VLCDLTKTGSGNTSVIKNPMSCPYQLSNNSVSFFLDNADSSQGSYFLCSLIFDPPPPQ 120
Db 61 VLCDLTKTGSGNTSVIKNPMSCPYQLSNNSVSFFLDNADSSQGSYFLCSLIFDPPPPQ 120

QY 121 EKNLSGGYLLIYESQLCCQLKWLPGCAAFVAALLFGCIFTWFAKKYRSVHDPNSE 180
Db 121 EKNLSGGYLLIYESQLCCQLKWLPGCAAFVAALLFGCIFTWFAKKYRSVHDPNSE 180

QY 181 YMFMAAVNTNKKSLAG 197
Db 181 YMFMAAVNTNKKSLAG 197

RESULT 3
Q9WVS0 PRELIMINARY; PRT; 200 AA.
ID Q9WVS0;
AC Q9WVS0;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
DE PRECURSOR (CCLP PRECURSOR) (SURFACE PROTEIN).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=INTESTINAL INTRA-EPITHELIAL;
RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
RA Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tefuri-Bladt A.,
RA Campbell P., Chang D., Chiu L., Dai T., Duncan G., Elliott G.S.,
RA Hui A., McCabe S.M., Scully S., Shaklee C.L., Van G., Mak T.W.,

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RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Tezuka K., Tamatani T.;
RT "Cell surface molecule mediating cell adhesion and signal
RT transmission.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RP STRAIN=BAUB/C; TISSUE=SPLEEN;
RC STRAIN=BAUB/C; TISSUE=SPLEEN;
RA Wu D., Giannoni M.A., Kiesecker C.L., Faas S.J., Mickie A.P.,
RA Matis L.A., Rother R.P.;
RT "CCLP, A novel molecule that regulates T cell activation.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RP STRAIN=BAUB/C; TISSUE=SPLEEN;
RC STRAIN=BAUB/C; TISSUE=SPLEEN;
RX MEDLINE=20225659; PubMed=10760791;
RA Mages H.W., Hutloff A., Heuck C., Buchner K., Himmelbauer H.,
RA Oliveri F., Kroccek R.A.;
RT "Molecular cloning and characterization of murine ICOS and
RT identification of B7h as ICOS ligand.";
RL Eur. J. Immunol. 30:1040-1047(2000).
DR EMBL; AB023132; BAA82126.1; -.
DR EMBL; AF257230; AAF70099.1; -.
DR EMBL; AJ250559; CAB71153.1; -.
DR MGD; MGI:1858745; ICOS.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 200 AA; 22690 MW; 9B2278E4CAB1DB47 CRC64;

Query Match 86.2%; Score 922; DB 11; Length 200;
Best Local Similarity 85.0%; Pred. No. 9.6e-91;
Matches 170; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 1 MKPYFCVFCFLIKLTGELNDLANHRMFSFHGGVQVSCNYPETVQOLKMLFKDRE 60
Db 1 MKPYFCVFCFLIKLTGELNDLANHRMFSFHGGVQVSCNYPETVQOLKMLFKDRE 60

QY 61 VLCDLTKTGSGNTSVIKNPMSCPYQLSNNSVSFFLDNADSSQGSYFLCSLIFDPPPPQ 120
Db 61 VLCDLTKTGSGNTSVIKNPMSCPYQLSNNSVSFFLDNADSSQGSYFLCSLIFDPPPPQ 120

QY 121 EKNLSGGYLLIYESQLCCQLKWLPGCAAFVAALLFGCIFTWFAKKYRSVHDPNSE 180
Db 121 EKNLSGGYLLIYESQLCCQLKWLPGCAAFVAALLFGCIFTWFAKKYRSVHDPNSE 180

QY 181 YMFMAAVNTNKKSLAGMTS 200
Db 181 YMFMAAVNTNKKSLAGMTS 200

RESULT 4
Q9JLI7 PRELIMINARY; PRT; 200 AA.
ID Q9JLI7;
AC Q9JLI7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CD28-RELATED PROTEIN 1 (INDUCIBLE COSTIMULATORY PROTEIN)
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=INTESTINAL INTRA-EPITHELIAL;
RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
RA Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tefuri-Bladt A.,
RA Campbell P., Chang D., Chiu L., Dai T., Duncan G., Elliott G.S.,
RA Hui A., McCabe S.M., Scully S., Shaklee C.L., Van G., Mak T.W.,

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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:26:25 ; Search time 75.12 Seconds
(without alignments)
295.724 Million cell updates/sec

Title: US-09-383-551B-14
Perfect score: 1076
Sequence: 1 MKPYFCHVFVFCFLIRLLTG.....YMFMAAVNTNKKSLRAGVTS 200

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Tc number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
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6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
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11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
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17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
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19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1076	100.0	200	19 AAW75958	Mouse cell surface
2	1063	98.8	200	21 AAY92212	Murine Th2-specific
3	1055	98.0	200	21 AAB08723	Amino acid sequenc
4	907	84.3	200	19 AAW71874	Rat cell surface p
5	897	83.4	216	19 AAW71875	Rat cell surface p
6	722.5	67.1	199	19 AAW75956	Human cell surface
7	722.5	67.1	199	19 AAW75957	Human cell surface
8	722.5	67.1	199	20 AAY08026	Human activated T-
9	722.5	67.1	199	21 AAB08731	Amino acid sequenc
10	722.5	67.1	199	22 AAE03428	Human gene 2 encod
11	722.5	67.1	199	22 AAE03460	Human gene 2 encod

12	722.5	67.1	199	22 AAE03525	Human secreted pro
13	707	65.7	198	21 AAY92213	Human Th2-specific
14	657	61.1	380	22 AAB67717	Amino acid sequenc
15	449.5	41.8	379	22 AAB67716	Amino acid sequenc
16	136	12.6	220	13 AAR20805	Human CD28 antigen
17	136	12.6	220	13 AAR27103	Sequence encoded b
18	136	12.6	220	17 AAW02131	Human CD28 CDNA pr
19	136	12.6	220	17 AAR91433	Human CD28 antigen
20	136	12.6	220	18 AAW38413	CD28. Homo sapien
21	136	12.6	220	19 AAW80442	Human CD28 antigen
22	136	12.6	220	20 AAW8451	Human CD28 antigen
23	136	12.6	220	21 AAY96128	Human cell surface
24	136	12.6	220	21 AAY44294	Human CD28 recepto
25	136	12.6	220	22 AAU02437	Human lymphocyte c
26	131.5	12.2	223	20 AAY41137	Human CD28 protein
27	131	12.2	221	21 AAY32286	Feline CD28. Feli
28	131	12.2	221	21 AAY32279	Cat CD28 receptor.
29	121	11.2	134	18 AAR35846	Human CD28 for use
30	121	11.2	152	16 AAR67706	CD28 extracellular
31	117	10.9	367	18 AAW35862	Human CD28:IgG2a c
32	116.5	10.8	225	20 AAY41136	Rat CD28 protein s
33	94.5	8.8	225	20 AAY41135	Mouse CD28 protein
34	85.5	7.9	633	21 AAB25541	Eucalyptus grandis
35	84.5	7.9	223	18 AAW25111	Soluble human CTLA
36	84.5	7.9	223	22 AAG66519	Human CTLA4. Homo
37	84.5	7.9	223	22 AAU00687	Human CTLA4 protei
38	82.5	7.7	223	21 AAY32287	Feline CTLA-4. Fe
39	82.5	7.7	223	21 AAY15129	Human CTLA-4 prote
40	82.5	7.7	223	21 AAY32280	Cat CTLA-4 recepto
41	81.5	7.6	117	20 AAY24469	Human CD28 gene pr
42	80.5	7.5	226	20 AAY41138	Chicken CD28 prote
43	80	7.4	168	19 AAW42340	CTLA-4 extracellul
44	79.5	7.4	187	19 AAR86945	Human T cell speci
45	79.5	7.4	187	19 AAW29728	Soluble CTLA4 muta

ALIGNMENTS

RESULT 1
AAW75958
ID AAW75958 standard; Protein; 200 AA.
XX
AC AAW75958;
XX
DT 11-DEC-1998 (first entry)
XX
DE Mouse cell surface protein.
XX
KW Mouse; cell surface protein; thymocyte; lymphocyte; cell adhesion;
KW signal transmission; autoimmune disorder; allergy; diagnosis;
KW mitogen-stimulated.
XX
OS Mus sp.
XX
PN W09838216-A1.
XX
PD 03-SEP-1998.
XX
PF 27-FEB-1998; 98WO-JP00837.
XX
PR 26-FEB-1998; 98JP-0062217.
PR 27-FEB-1997; 97JP-0062290.
XX
PA (NIBS) JAPAN TOBACCO INC.
XX
PI Tamatani T, Tezuka K;
XX
DR WPI; 1998-481144/41.
XX
DR N-PSDB; AAV53200.
XX
PT Cell surface molecule expressed in thymocytes and lymphocytes and
PT mediating signal transmission and cell adhesion, and antibodies to

PT it useful in treatment of auto-immune and allergic disorders.

PS Claim 9; Page 110-112; 149pp; Japanese.

XX The present sequence represents a mouse cell surface protein which is
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
 CC antibodies recognising the cell surface protein. These antibodies also
 CC produce an increase in peripheral blood lymphocytes in the presence of
 CC an antibody recognising CD3 antigen. The cell surface protein contains
 CC the amino acid sequence FPPPPF in its extracellular region and the
 CC sequence YMF in its intracellular region. The cell surface protein can
 CC be used in the prevention and treatment of auto-immune and allergic
 CC diseases, and in the diagnosis and investigation of such disorders.

XX Sequence 200 AA;

Query Match 100.0%; Score 1076; DB 19; Length 200;

Best Local Similarity 100.0%; Pred. No. 4.4e-115; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPYFCHVFVFCFLRLTGEINGSADHRMFSFHNGVQISCKYPETVQOLKMLRFRERE 60

DB 1 mkpyfchvfvcflrltgeingsadhrmfsfhngvgvisckypetvqqlkmrlfrere 60

QY 61 VLCELTKTGSGNAVSIRKPNMCLVHLNNSVSFFLNPNDSQSGSYFCSLSIFDPPPPQ 120

DB 61 vlceltktkgsgnavsikpnmlclvhlslnsvsfflnpdsqsgsyfcslsifdppppq 120

QY 121 ERNLSSGYLHYESQLCCQLKWLPGVLPFAFVVLLFGCILLIWFSSKKYSSVHDPNSE 180

DB 121 ernlsggylyhiesqlccqlkwlpgvlpafvfvllfgcilliwfskkyssvhdnpse 180

QY 181 YMFMAAVNTNKKSRLAGVTS 200

DB 181 ymfmaavntnkkksrlagvts 200

RESULT 2

AA92212 2
 ID AA92212 standard; Protein; 200 AA.

AC AA92212;

DT 10-AUG-2000 (first entry)

XX Murine Th2-specific polypeptide, m1228.

XX m1288; Th2-specific; T helper cell; anti-inflammatory; antiarthritic;
 KW CD28; antidiabetic; immunosuppressive; neuroprotective; dermatological;
 KW antipsoriatic; antiasthmatic; antiallergic; anti-viral; ophthalmological;
 KW CTLA-4; nephrotropic; anti-HIV; antibacterial.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 114..119

FT /label= conserved_PPP_motif

FT /note= "common in CD28 and CTLA-4"

FT Peptide 181..184

FT /label= YXXM_motif

FT /note= "common in CD28 and CTLA-4; necessary for
 CD28-mediated phosphatidylinositol 3-kinase
 activity"

XX WO200019988-A1.

PN 13-APR-2000.

PD 06-OCT-1999; 99WO-US23156.

XX 07-OCT-1998; 98US-0168229.

PR

PR 26-FEB-1999; 99US-0258670.

PR 06-OCT-1999; 99US-0413136.

XX (MILL-) MILLENNIUM PHARM INC.

XX Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J;

XX WPI; 2000-303619/26.

XX N-PSDB; AAA09054.

XX T helper (Th) 2 nucleic acids and encoded proteins, useful for the
 FT diagnosis and treatment of immune and respiratory disorders such as
 FT Crohn's diseases, arthritis, insulin dependent diabetes and
 FT autoimmunity

XX Claim 16; Page 130-131; 159pp; English.

XX This Th2-specific polypeptide is encoded by a murine orthologue m1288.
 CC The protein shares homology with both human and murine CD28 and CTLA-4.
 CC A novel method for modulating a Th2 response, an immune response, or
 CC suppressing airway inflammation or hyperresponsiveness in a mammal
 CC comprises administering a Th2-specific polypeptide of the invention, an
 CC antibody to such a polypeptide or allelic variants of the genes. The
 CC novel DNA and polypeptide sequences are useful for treatment and
 CC diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases,
 CC arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis,
 CC dermatitis, psoriasis, graft rejection, graft versus host diseases,
 CC sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis,
 CC viral infections (including human immunodeficiency virus (HIV)),
 CC bacterial infections, bronchitis, cystic fibrosis, diphtheria,
 CC emphysema, pneumonia, and Legionnaires disease.

XX Sequence 200 AA;

Query Match 98.8%; Score 1063; DB 21; Length 200;

Best Local Similarity 99.0%; Pred. No. 1.4e-113;

Matches 198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKPYFCHVFVFCFLRLTGEINGSADHRMFSFHNGVQISCKYPETVQOLKMLRFRERE 60

DB 1 mkpyfchvfvcflrltgeingsadhrmfsfhngvgvisckypetvqqlkmrlfrere 60

QY 61 VLCELTKTGSGNAVSIRKPNMCLVHLNNSVSFFLNPNDSQSGSYFCSLSIFDPPPPQ 120

DB 61 vlceltktkgsgnavsikpnmlclvhlslnsvsfflnpdsqsgsyfcslsifdppppq 120

QY 121 ERNLSSGYLHYESQLCCQLKWLPGVLPFAFVVLLFGCILLIWFSSKKYSSVHDPNSE 180

DB 121 ernlsggylyhiesqlccqlkwlpgvlpafvfvllfgcilliwfskkyssvhdnpse 180

QY 181 YMFMAAVNTNKKSRLAGVTS 200

DB 181 ymfmaavntnkkksrlagvts 200

RESULT 3

AA08723

ID AA08723 standard; Protein; 200 AA.

AC AA08723;

DT 02-JAN-2001 (first entry)

XX Amino acid sequence of a murine CRP1 polypeptide.

XX CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;

KW T-lymphocyte activation; type I transmembrane protein; T cell activation;

KW T cell proliferation; T-cell mediated disorder.

XX Mus sp.

XX

XX Key Location/Qualifiers

XX

FT Peptide 1..20
 FT /note= "signal peptide"
 FT Protein 21..200
 FT /note= "mature protein"
 FT Domain 21..145
 FT /note= "extracellular domain"
 FT Domain 146..163
 FT /note= "predicted transmembrane domain"
 FT Domain 164..200
 FT /note= "intracellular domain"
 XX WO200046240-A2.
 PN 10-AUG-2000.
 XX 27-JAN-2000; 2000WO-US01871.
 PF 03-FEB-1999; 99US-0244448.
 PR 08-MAR-1999; 99US-0264527.
 XX (AMGE-) AMGEN INC.
 XX Yoshinaga SK;
 PI WPI; 2000-543476/49.
 DR N-PSDB; AAA64554.
 XX Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
 PT in the treatment, prevention and diagnosis of T cell mediated disorders
 PT
 XX Claim 11; Fig 1A; 174pp; English.
 PS
 XX The present sequence represents a CRP1 (CD28 related protein-1)
 CC polypeptide. The specification also describes a B7RP1 (B7 related
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
 CC predicted to be a type I transmembrane protein. The nucleic acids are
 CC useful for regulating T cell activation or proliferation in an animal.
 CC The polypeptides are useful for treating, preventing ameliorating or
 CC diagnosing a T-cell mediated disorder in an animal. They can also be
 CC used to identify test molecules that bind to the polypeptides.
 XX
 SQ Sequence 200 AA;

Query Match 98.0%; Score 1055; DB 21; Length 200;
 Best Local Similarity 98.5%; Pred. No. 1.1e-112;
 Matches 197; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKPYCHVVFVFCFLIRLLTGEINGSADHRMFSFHNGGVOISCKYPTVQOLKMLFRERE 60
 DB 1 mkpyfcrvfvfcflirlltgeingsadhrmfsfhnggvqiskypetvqqlkmfrere 60
 QY 61 VLCELTKTGSGNAVSINKNPMCLCYHLNSNVSFFLNPDSSQGSYFCSLSIFDPPPFQ 120
 DB 61 vlceltktkgsgnavsiknpmlclcyhlnsnvsfflnpdssqgsyfcslsifdpppfq 120
 QY 121 ERNLGGYLIHYESQICCOLKWLPLVGLPFAFVYVLLFGCILIIWFSKKYGSVHPDNPSE 180
 DB 121 ernlsgglylhyesqiccolkwlplvglpfaafvvyvllfgciliwfskkygssvhdnpse 180
 QY 181 YMFMAAVNTNKKSRLAGVTS 200
 DB 181 ymfmaavntnkkslragvts 200
 RESULT 4
 ID AAW71874
 XX AAW71874 standard; Protein; 200 AA.
 AC AAW71874;
 XX

DT 11-DEC-1998 (first entry)
 XX Rat cell surface protein #1.
 DE Rat; cell surface protein; thymocyte; lymphocyte; cell adhesion;
 KW signal transmission; autoimmune disorder; allergy; diagnosis;
 KW mitogen-stimulated.
 XX Rattus sp.
 OS WO9838216-A1.
 PN 03-SEP-1998.
 XX 27-FEB-1998; 98WO-JP00837.
 PF 26-FEB-1998; 98JP-0062217.
 PR 27-FEB-1997; 97JP-0062290.
 XX (NISR) JAPAN TOBACCO INC.
 PA Tamatani T, Tezuka K;
 PI WPI; 1998-481144/41.
 DR N-PSDB; AAV61357.
 XX Cell surface molecule expressed in thymocytes and lymphocytes and -
 PT mediating signal transmission and cell adhesion, and antibodies to
 PT it useful in treatment of autoimmune and allergic disorders.
 XX Claim 9; Page 106-109; 149pp; Japanese.
 PS
 XX The present sequence represents a rat cell surface protein which is
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
 CC antibodies recognising the cell surface protein. These antibodies also
 CC produce an increase in peripheral blood lymphocytes in the presence of
 CC an antibody recognising CD3 antigen. The cell surface protein contains
 CC the amino acid sequence FDPFPF in its extracellular region and the
 CC sequence YNFM in its intracellular region. The cell surface protein can
 CC be used in the prevention and treatment of autoimmune and allergic
 CC diseases, and in the diagnosis and investigation of such disorders.
 XX
 SQ Sequence 200 AA;

Query Match 84.3%; Score 907; DB 19; Length 200;
 Best Local Similarity 84.0%; Pred. No. 1.1e-95;
 Matches 168; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 MKPYCHVVFVFCFLIRLLTGEINGSADHRMFSFHNGGVOISCKYPTVQOLKMLFRERE 60
 DB 1 mkpyfcrvfvfcflirlltgeindlanhrmfsfhnggvqiscnypetvqqlkmfkdre 60
 QY 61 VLCELTKTGSGNAVSINKNPMCLCYHLNSNVSFFLNPDSSQGSYFCSLSIFDPPPFQ 120
 DB 61 vlceltktkgsgnavsiknpmlclcyhlnsnvsfflnpdssqgsyfcslsifdpppfq 120
 QY 121 ERNLGGYLIHYESQICCOLKWLPLVGLPFAFVYVLLFGCILIIWFSKKYGSVHPDNPSE 180
 DB 121 ernlsgglylhyesqiccolkwlplvglpfaafvvyvllfgciliwfskkygssvhdnpse 180
 QY 181 YMFMAAVNTNKKSRLAGVTS 200
 DB 181 ymfmaavntnkkslragmts 200
 RESULT 5
 ID AAW71875
 XX AAW71875 standard; Protein; 216 AA.
 AC AAW71875;
 XX

DT 11-DEC-1998 (first entry)
 XX Rat cell surface protein #2.
 DE
 XX
 KW Rat; cell surface protein; thymocyte; lymphocyte; cell adhesion;
 KW signal transmission; autoimmune disorder; allergy; diagnosis;
 KW mitogen-stimulated.
 XX
 OS Rattus sp.
 XX
 XX WO9838216-A1.
 PN
 XX 03-SEP-1998.
 PD
 XX 27-FEB-1998; 98WO-JP00837.
 PF
 XX 26-FEB-1998; 98JP-0062217.
 PR
 PR 27-FEB-1997; 97JP-0062290.
 XX
 XX (NISR) JAPAN TOBACCO INC.
 PA
 XX Tamatani T, Tezuka K;
 PI
 XX WPI; 1998-481144/41.
 DR
 DR N-PSDB; AAV61358.
 XX
 PT Cell surface molecule expressed in thymocytes and lymphocytes and -
 PT mediating signal transmission and cell adhesion, and antibodies to
 PT it useful in treatment of autoimmune and allergic disorders.
 XX
 XX Claim 9; Page 112-115; 149pp; Japanese.
 PS
 XX The present sequence represents a rat cell surface protein which is
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
 CC antibodies recognising the cell surface protein. These antibodies also
 CC produce an increase in peripheral blood lymphocytes in the presence of
 CC an antibody recognising CD3 antigen. The cell surface protein contains
 CC the amino acid sequence FDPDPF in its extracellular region and the
 CC sequence YMF in its intracellular region. The cell surface protein can
 CC be used in the prevention and treatment of autoimmune and allergic
 CC diseases, and in the diagnosis and investigation of such disorders.
 XX
 SQ Sequence 216 AA;
 Query Match 83.4%; Score 897; DB 19; Length 216;
 Best Local Similarity 84.3%; Pred. No. 1.7e-94;
 Matches 166; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
 QY 1 MKPYFCHVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPTVQOLKMLFRERE 60
 DB 1 mkpyfscvfvfclllkllgeindlanhrmfshdggvqiscnypetvqqlkmqlfkdre 60
 QY 61 VLCELTKTGSGNAVSINKPMCLYHLSNNSVSFFLNPNDSQSGSYFYFCSLIFDPPPFQ 120
 DB 61 vlcdltktkgsgntvsiknpsmcpyqlsnnsvsfflnhdadsggyfclslsifdpppfq 120
 QY 121 ERNLGGYLHIYESQCCOLKWLPLVGLPAFVVLVLFGLIILWFSKKYKGSVHDPNSE 180
 DB 121 exnl99gylllyesqlccqklwlpvgcaafvaallfgcivfwfakkyrsvhdnpse 180
 QY 181 YMFMAAVNTNKKSRLAG 197
 DB 181 ymfmaavntnkkrsrlag 197
 RESULT 6
 ID AAW75956
 XX AAW75956 standard; Protein; 199 AA.
 AC AAW75956;
 XX

DT 11-DEC-1998 (first entry)
 XX Human cell surface protein #1.
 DE
 XX
 KW Human; cell surface protein; thymocyte; lymphocyte; cell adhesion;
 KW signal transmission; autoimmune disorder; allergy; diagnosis;
 KW mitogen-stimulated.
 XX
 OS Homo sapiens.
 XX
 XX WO9838216-A1.
 PN
 XX 03-SEP-1998.
 PD
 XX 27-FEB-1998; 98WO-JP00837.
 PF
 XX 26-FEB-1998; 98JP-0062217.
 PR
 PR 27-FEB-1997; 97JP-0062290.
 XX
 XX (NISR) JAPAN TOBACCO INC.
 PA
 XX Tamatani T, Tezuka K;
 PI
 XX WPI; 1998-481144/41.
 DR
 DR N-PSDB; AAV53198.
 XX
 PT Cell surface molecule expressed in thymocytes and lymphocytes and -
 PT mediating signal transmission and cell adhesion, and antibodies to
 PT it useful in treatment of autoimmune and allergic disorders.
 XX
 XX Claim 2; Page 99-101; 149pp; Japanese.
 PS
 XX The present sequence represents a human cell surface protein which is
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
 CC antibodies recognising the cell surface protein. These antibodies also
 CC produce an increase in peripheral blood lymphocytes in the presence of
 CC an antibody recognising CD3 antigen. The cell surface protein contains
 CC the amino acid sequence FDPDPF in its extracellular region and the
 CC sequence YMF in its intracellular region. The cell surface protein can
 CC be used in the prevention and treatment of autoimmune and allergic
 CC diseases, and in the diagnosis and investigation of such disorders.
 XX
 SQ Sequence 199 AA;
 Query Match 67.1%; Score 722.5; DB 19; Length 199;
 Best Local Similarity 68.3%; Pred. No. 1.6e-74;
 Matches 136; Conservative 20; Mismatches 42; Indels 1; Gaps 1;
 QY 1 MKPYFCHVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPTVQOLKMLFRERE 60
 DB 1 mksqglwyfflclrlkvlgtgeingsanyemflhmgvgvqlckypdivqqlkmgllk99q 60
 QY 61 VLCELTKTGSGNAVSINKPMCLYHLSNNSVSFFLNPNDSQSGSYFYFCSLIFDPPPFQ 120
 DB 61 ilcdltktkgsgntvsikalkfchsqslsnnsvsfflynldshanyfynlsifdpppfk 120
 QY 121 ERNLGGYLHIYESQCCOLKWLPLVGLPAFVVLVLFGLIILWFSKKYKGSVHDPNSE 180
 DB 121 v-rltggylhiyesqlccqklwlpigcaafvvvcilgciliclwltkkyssvhdnpge 179
 QY 181 YMFMAAVNTNKKSRLAGVT 199
 DB 180 ymfmravntakksrltdvt 198
 RESULT 7
 ID AAW75957
 XX AAW75957 standard; Protein; 199 AA.
 AC AAW75957;
 XX

DT 11-DEC-1998 (first entry)
 XX Human cell surface protein #2.
 DE
 XX Human; cell surface protein; thymocyte; lymphocyte; cell adhesion;
 KW signal transmission; autoimmune disorder; allergy; diagnosis;
 KW mitogen-stimulated.
 KW
 XX Homo sapiens.
 OS
 XX WO9838216-A1.
 PN
 XX 03-SEP-1998.
 XX
 XX 27-FEB-1998; 98WO-JP00837.
 PF
 XX 26-FEB-1998; 98JP-0062217.
 PR
 XX 27-FEB-1997; 97JP-0062290.
 XX
 XX (NISE) JAPAN TOBACCO INC.
 PA
 XX Tamatani T, Tezuka K;
 XX WPI: 1998-481144/41.
 DR
 XX N-PSDB; AAV53199.
 XX
 XX Cell surface molecule expressed in thymocytes and lymphocytes and -
 PT mediating signal transmission and cell adhesion, and antibodies to
 PT it useful in treatment of auto-immune and allergic disorders.
 XX
 XX Claim 9; Page 101-105; 149pp; Japanese.
 PS
 XX The present sequence represents a human cell surface protein which is
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
 CC antibodies recognising the cell surface protein. These antibodies also
 CC produce an increase in peripheral blood lymphocytes in the presence of
 CC an antibody recognising CD3 antigen. The cell surface protein contains
 CC the amino acid sequence FDRPPF in its extracellular region and the
 CC sequence YMF in its intracellular region. The cell surface protein can
 CC be used in the prevention and treatment of autoimmune and allergic
 CC diseases, and in the diagnosis and investigation of such disorders.
 XX
 XX Sequence 199 AA;
 SQ
 Query Match 67.1%; Score 722.5; DB 19; Length 199;
 Best Local Similarity 68.3%; Pred. No. 1.6e-74;
 Matches 136; Conservative 20; Mismatches 42; Indels 1; Gaps 1;
 QY 1 MKPYFCHVFCELIIRLLTGEINGSADHRMFSFHNGGVQISCKYPTVQOLKMLRFRERE 60
 DB - 1 mksglwyfflclrlkvtlgeingsanyemfifhngvgqilckypdivqgkmlkkgg 60
 QY 61 VLCELTKTGGSNVAGSIKNPMLCLYHLNNSVSFFLNPDSSQGSYVFCSLSFDPDPFQ 120
 DB 61 icdlctksgntsvsiksikfchsqslmsvfflylnldshanyfncslsfidpppfk 120
 QY 121 ERNLGGYLHIYESQLCCQLKWLPLVGLPAFVVLVLLFGCILIIWFSKKYKSSVHDPNSE 180
 DB 121 v-tltggylhiesqicccqlkfwlpigcaafvvcilgcilicwltckkkyssvhdnpge 179
 QY 181 YMFMAAVNTNKSRLAGVT 199
 DB 180 ymfmravntakksrltdvt 198
 RESULT 8
 AAY08026
 ID AAY08026 standard; Protein; 199 AA.
 XX
 AC AAY08026;
 XX

DT 08-JUL-1999 (first entry)
 XX Human activated T-lymphocyte protein 8F4.
 DE
 XX T-lymphocyte; human; 8F4; T cell co-stimulation; activated; CD4+; CD8+;
 KW anticancer; antiviral; anti-asthma; immunomodulator; proliferation;
 KW T cell activation; cytokine synthesis; regulatory element; B cell;
 KW T cell-dependent antibody production; treatment; prevention; cancer;
 KW autoimmune disease; transplant rejection; immune system regulation;
 KW disorder; acquired immune deficiency syndrome; AIDS; asthma.
 XX
 OS Homo sapiens.
 XX
 XX WO9915553-A2.
 PN
 XX 01-APR-1999.
 XX
 XX 23-SEP-1998; 98WO-DE02896.
 PF
 XX 11-MAY-1998; 98DE-1021060.
 PR
 XX 23-SEP-1997; 97DE-1041929.
 XX
 XX (DEKO-) DEUT KOCH INST ROBERT.
 PA (BUND) BUNDESREPUBLIK DEUT PAUL-EHRlich-INST.
 XX
 XX Krocze R;
 PI
 XX WPI: 1999-276975/23.
 DR
 XX N-PSDB; AAX37661.
 XX
 XX Polypeptide 8F4 co-stimulates T cells and is present only on
 PT activated cells
 PT
 XX Claim 2; Page 24; 47pp; German.
 PS
 XX This invention describes a novel human protein, 8F4, and its encoding
 CC nucleic acid which co-stimulates T cells and is present on activated CD4+
 CC and CD8+ T cells but not on resting or activated B cells, granulocytes,
 CC monocytes, natural killer or dendritic cells. 8F4 has anticancer,
 CC antiviral, anti-asthma and immunomodulatory activity. 8F4 provides a
 CC strong co-stimulatory signal for T cell activation, i.e. it amplifies
 CC proliferation of T cells, synthesis of certain cytokines and other
 CC regulatory agents, and improves T cell-dependent antibody production
 CC by B cells. Agents that inhibit 8F4 are used to treat or prevent
 CC autoimmune diseases, to prevent transplant rejection and to treat
 CC disorders of immune system regulation. 8F4, or cells that express it,
 CC is/are used to treat or prevent cancers, acquired immune deficiency
 CC syndrome, asthma and chronic infectious diseases (e.g. hepatitis B or C).
 XX
 XX Sequence 199 AA;
 SQ
 Query Match 67.1%; Score 722.5; DB 20; Length 199;
 Best Local Similarity 68.3%; Pred. No. 1.6e-74;
 Matches 136; Conservative 20; Mismatches 42; Indels 1; Gaps 1;
 QY 1 MKPYFCHVFCELIIRLLTGEINGSADHRMFSFHNGGVQISCKYPTVQOLKMLRFRERE 60
 DB - 1 mksglwyfflclrlkvtlgeingsanyemfifhngvgqilckypdivqgkmlkkgg 60
 QY 61 VLCELTKTGGSNVAGSIKNPMLCLYHLNNSVSFFLNPDSSQGSYVFCSLSFDPDPFQ 120
 DB 61 icdlctksgntsvsiksikfchsqslmsvfflylnldshanyfncslsfidpppfk 120
 QY 121 ERNLGGYLHIYESQLCCQLKWLPLVGLPAFVVLVLLFGCILIIWFSKKYKSSVHDPNSE 180
 DB 121 v-tltggylhiesqicccqlkfwlpigcaafvvcilgcilicwltckkkyssvhdnpge 179
 QY 181 YMFMAAVNTNKSRLAGVT 199
 DB 180 ymfmravntakksrltdvt 198

CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies, asthma;
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 CC angiotensin-related disorders, kidney disorders, gastrointestinal disorders,
 CC pregnancy-related disorders, endocrine disorders, and infections. The
 CC proteins can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues, to identify their cognate ligands or binding
 CC partners, and in chemotaxis, and can be used as a food additive or
 CC preservative to modify storage properties. Antibodies specific for a
 CC protein of the invention can be used in alleviating symptoms associated
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
 CC The present sequence represents a human secreted protein of
 CC the invention.
 XX
 S0 Sequence 199 AA;

Query Match 67.1%; Score 722.5; DB 22; Length 199;
 Best Local Similarity 68.3%; Pred. No. 1.6e-74;
 Matches 136; Conservative 20; Mismatches 42; Indels 1; Gaps 1;
 QY 1 MKPYFCHVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPTVQOLKMLFRERE 60
 Db 1 mksglwyfflclrlkvlkgeingsanyemfifhnggvqlckypdivqfkmqlkqgg 60
 QY 61 VLCELTKTGSGNAVSINKPMCLVHLSNNSVSFFLNPNDSOGSYFCSLSIFDPPFPQ 120
 Db 61 ilcdltktgsgntvsiklckfchsglsnnsvsfflnldshanyffcnlsifdpppfk 120
 QY 121 ERNLGGYLHIYESQLCCOLKWLPLVGLPAFVVVLLFGCILLIWFSSKKYGSVHDNPSE 180
 Db 121 v-tltggyihiesqlccqlkfwlpigcaafvvcilgcilclwtkkkyssvhdnpge 179
 QY 181 YMFMAAVNTNKKSLRAGVT 199
 Db 180 ymfmravntakksrltdvt 198

RESULT 11
 AAE03460
 ID AAE03460 standard; Protein; 199 AA.
 AC AAE03460;
 XX
 DE 0-AUG-2001 (first entry)
 XX Human gene 2 encoded secreted protein HT2SG64, SEQ ID NO: 143.
 KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
 KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
 KW inflammation; neurological disorder; Alzheimer's disease; food additive;
 KW angiotensin-related disorder; kidney disorder; gastrointestinal disorder; allergy;
 KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
 KW cell culture; chemotaxis; vulnerability; binding partner identification;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Location/Qualifiers
 FT 1..19 /label= signal_peptide
 FT 20..199 /note= "Mature human secreted protein"
 FT
 XX WO200132675-A1.

XX
 PD 10-MAY-2001.
 XX 25-OCT-2000; 2000WO-US29363.
 XX 29-OCT-1999; 990US-0162239.
 PR 30-JUN-2000; 2000US-0215139.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Ruben SM, Komatsoulis GA, Wei P, Baker KP, Young PE;
 PI WPI; 2001-328772/34.
 DR N-PSDB; AAD07842.
 XX Thirty two human secreted proteins, useful for treating cancers,
 PT hyperproliferative disorders, inflammatory disorders, neurological
 PT disorders, autoimmune diseases and cardiovascular disorders -
 XX
 XX Claim 11; Page 489-490; 576pp; English.
 PS
 XX AAD07809-AAD07907 represent cDNAs corresponding to 32 human secreted
 CC protein genes, and AAE03427-AAE03523 represent the proteins they encode.
 CC AAE03524-AAE03537 represent human secreted protein fragments or variants.
 CC The secreted proteins and their genes are useful for preventing, treating
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.
 CC Pathological conditions can be diagnosed by determining the amount of the
 CC new protein in a sample or by determining the presence of mutations in
 CC the new genes. Specific uses are described for each of the 32 genes,
 CC based on the tissues in which they are most highly expressed, and include
 CC developing products for the diagnosis or treatment of proliferative
 CC disorders, cancer, tumours, foetal and developmental abnormalities,
 CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 CC angiotensin-related disorders, kidney disorders, gastrointestinal disorders,
 CC pregnancy-related disorders, endocrine disorders, and infections. The
 CC proteins can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues, to identify their cognate ligands or binding
 CC partners, and in chemotaxis, to identify their cognate ligands or binding
 CC to regenerate tissues, to identify their cognate ligands or binding
 CC partners, and in chemotaxis, and can be used as a food additive or
 CC preservative to modify storage properties. Antibodies specific for a
 CC protein of the invention can be used in alleviating symptoms associated
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
 CC The present sequence represents a human secreted protein of
 CC the invention.
 XX
 S0 Sequence 199 AA;

Query Match 67.1%; Score 722.5; DB 22; Length 199;
 Best Local Similarity 68.3%; Pred. No. 1.6e-74;
 Matches 136; Conservative 20; Mismatches 42; Indels 1; Gaps 1;
 QY 1 MKPYFCHVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPTVQOLKMLFRERE 60
 Db 1 mksglwyfflclrlkvlkgeingsanyemfifhnggvqlckypdivqfkmqlkqgg 60
 QY 61 VLCELTKTGSGNAVSINKPMCLVHLSNNSVSFFLNPNDSOGSYFCSLSIFDPPFPQ 120
 Db 61 ilcdltktgsgntvsiklckfchsglsnnsvsfflnldshanyffcnlsifdpppfk 120
 QY 121 ERNLGGYLHIYESQLCCOLKWLPLVGLPAFVVVLLFGCILLIWFSSKKYGSVHDNPSE 180
 Db 121 v-tltggyihiesqlccqlkfwlpigcaafvvcilgcilclwtkkkyssvhdnpge 179
 QY 181 YMFMAAVNTNKKSLRAGVT 199
 Db 180 ymfmravntakksrltdvt 198

CC The present sequence represents a human secreted protein variant
CC referred to in the disclosure of the invention.
XX
SQ Sequence 199 AA;

Query Match 67.1%; Score 722.5; DB 22; Length 199;
Best Local Similarity 68.3%; Pred. No. 1.6e-74;
Matches 136; Conservative 20; Mismatches 42; Indels 1; Gaps 1;

QY 1 MKPYFCHVFVFCFLIRLLTGEINGSADHRMFSEHNGGVOISCKYPTVQOLKMLRFRERE 60
|| : ||| : ||| ||||| : || ||||| |||| : || ||| :
Db 1 mksglwyfflclrlkvtlgeingsanyemfihngvgqilckypdivgfkmlkqgq 60

QY 61 VLCELTKTGSGNAVSIKNPMLCLVHLNNSVSFFLNPNPDSSOGSYVFCSLSTFDPPFPQ 120
||| : ||| ||||| ||||| : ||| ||||| ||||| : ||| : ||| ||||| :
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QY 121 ERNLGGYLHIYESQLCCQLKWLVPGLPAFVVLVFLFGCILIIWFSKKYKGSVHDPNSE 180
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Db 121 v-tlggylhiyesqlccqlkfwlpigcaafvvcilgcilicwtckkkyssvhdnpge 179

QY 181 YMFMAAVNTNKKSLAGVT 199
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Db 180 ymfmravntakksrldtvt 198

RESULT 13
AA92213
ID AAY92213 standard; Protein; 198 AA.
XX
AC AAY92213;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human Th2-specific polypeptide, h1228.
XX
KW h1228; Th2-specific; T helper cell; anti-inflammatory; antiarthritic;
KW CD28; antidiabetic; immunosuppressive; neuroprotective; dermatological;
KW antipsoriatic; antiasthmatic; antiallergic; anti-viral; ophthalmological;
KW CTLA-4; nephrotropic; anti-HIV; antibacterial.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT /label= conserved_PPP_motif
FT /note= "common in CD28 and CTLA-4"
FT 178..181
FT /label= YXXM_motif
FT /note= "common in CD28 and CTLA-4; necessary for
FT CD28-mediated phosphatidylinositol 3-kinase
FT activity"
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WO200019988-A1.
XX
13-APR-2000.
XX
06-OCT-1999; 99WO-US23156.
XX
07-OCT-1998; 98US-0168229.
XX
26-FEB-1999; 99US-0258670.
XX
06-OCT-1999; 99US-0413136.
XX
(MILL-) MILLENNIUM PHARM INC.
XX
Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J;
XX
WPI: 2000-303619/26.
XX
N-PSDB; AAA09056.
XX
T helper (Th) 2 nucleic acids and encoded proteins, useful for the
XX diagnosis and treatment of immune and respiratory disorders such as

RESULT 12
AAE03525
ID AAE03525 standard; Protein; 199 AA.
XX
AC AAE03525;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human secreted protein variant, SEQ ID NO: 211.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW inflammation; neurological disorder; Alzheimer's disease; food additive;
KW anglogenetic disorder; kidney disorder; gastrointestinal disorder; allergy;
KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW cell culture; chemotaxis; vulnery; binding partner identification;
KW
XX
OS Homo sapiens.
XX
PN WO200132675-A1.
XX
PD 10-MAY-2001.
XX
PF 25-OCT-2000; 2000WO-US29363.
XX
PR 29-OCT-1999; 99US-0162239.
XX
PR 30-JUN-2000; 2000US-0215139.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Komatsoulis GA, Wel P, Baker KP, Young PE;
XX
WPI: 2001-328772/34.
XX
XX Thirty two human secreted proteins, useful for treating cancers,
PT hyperproliferative disorders, inflammatory disorders, neurological
PT disorders, autoimmune diseases and cardiovascular disorders -
XX
Disclosure; Page 524; 576pp; English.
XX
AA07809-AAD07907 represent cDNAs corresponding to 32 human secreted
XX protein genes, and AAE03427-AAE03523 represent the proteins they encode.
XX AAE03524-AAE03537 represent human secreted protein fragments or variants.
XX The secreted proteins and their genes are useful for preventing, treating
XX or ameliorating medical conditions, e.g., by protein or gene therapy.
XX Pathological conditions can be diagnosed by determining the amount of the
XX new protein in a sample or by determining the presence of mutations in
XX the new genes. Specific uses are described for each of the 32 genes,
XX based on the tissues in which they are most highly expressed, and include
XX developing products for the diagnosis or treatment of proliferative
XX disorders, cancer, tumours, foetal and developmental abnormalities,
XX haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
XX diseases (e.g., rheumatoid arthritis), inflammation, allergies,
XX neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
XX cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
XX psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
XX anglogenetic disorders, kidney disorders, gastrointestinal disorders,
XX pregnancy-related disorders, endocrine disorders, and infections. The
XX proteins can also be used to aid wound healing and epithelial cell
XX proliferation, to prevent skin aging due to sunburn, to maintain organs
XX before transplantation, for supporting cell culture of primary tissues,
XX to regenerate tissues, to identify their cognate ligands or binding
XX partners, and in chemotaxis, and can be used as a food additive or
XX preservative to modify storage properties. Antibodies specific for a
XX protein of the invention can be used in alleviating symptoms associated
XX with the disorders mentioned above, and in diagnostic immunoassays e.g.,
XX radioimmunoassay or enzyme linked immunosorbent assay (ELISA).

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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:27:00 : Search time 28.8 Seconds
(without alignments)
169.622 Million cell updates/sec

Title: US-09-383-551B-14

Perfect score: 1076

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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T number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	132.5	12.3	218	3	US-08-228-208A-20
2	132	12.3	220	3	US-08-228-208A-21
3	131.5	12.2	223	1	US-08-505-058-5
4	131.5	12.2	223	2	US-08-459-818-25
5	131.5	12.2	223	2	US-08-889-666-25
6	131.5	12.2	223	2	US-08-465-078-25
7	131.5	12.2	223	2	US-08-725-776-25
8	131.5	12.2	223	3	US-08-488-062-25
9	121	11.2	134	3	US-08-630-172-3
10	121	11.2	134	4	US-09-375-419-3
11	117	10.9	367	3	US-08-630-172-19
12	117	10.9	367	4	US-09-375-419-19
13	116.5	10.8	225	1	US-08-505-058-4
14	116.5	10.8	225	2	US-08-459-818-24
15	116.5	10.8	225	2	US-08-889-666-24
16	116.5	10.8	225	2	US-08-465-078-24
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24	94.5	8.8	225	2	US-08-465-078-23
25	94.5	8.8	225	2	US-08-725-776-23
26	94.5	8.8	225	2	US-08-488-062-23
27	82.5	7.7	223	3	US-08-228-208A-17

28 81.5 7.6 117 2 US-08-529-878B-39 Sequence 39, Appl
29 81.5 7.6 221 3 US-08-228-208A-22 Sequence 22, Appl
30 80.5 7.5 226 1 US-08-505-058-6 Sequence 6, Appl
31 80.5 7.5 226 2 US-08-459-818-26 Sequence 26, Appl
32 80.5 7.5 226 2 US-08-889-666-26 Sequence 26, Appl
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35 80.5 7.5 226 2 US-08-488-062-26 Sequence 26, Appl
36 79.5 7.4 187 1 US-08-067-684-14 Sequence 14, Appl
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41 79.5 7.4 187 2 US-08-725-776-14 Sequence 14, Appl
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43 79.5 7.4 187 3 US-08-228-208A-14 Sequence 14, Appl
44 79.5 7.4 187 5 PCT-US95-06726-36 Sequence 36, Appl
45 77 7.2 124 3 US-08-630-172-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-228-208A-20
; Sequence 20, Application US/08228208A
; Patent No. 6090914
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Wallace, Philip M.
; TITLE OF INVENTION: CTLA4/CD28Ig HYBRID FUSION
; TITLE OF INVENTION: PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,208A
; FILING DATE: 15-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-30US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310 445-1140
; TELEFAX: 310 445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-228-208A-20

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78 VYSKTGFCDCGLNESVTFYQLNLYNQTDIYFCKTEVMYPPYLDNEKSNGTIHHVKG 137
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; Sequence 5, Application US/08505058
; Patent No. 5773253

; PATENT NO. 5773233
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 ; GENERAL INFORMATION:
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 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Peach, Robert
 ;

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; TITLE OF INVENTION: CTLA4 Mutant Molecules and Uses Thereof
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; INVENTOR: RECH, ROBERT
;
; NUMBER OF SEQUENCES: 13
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Merchant & Gould
;

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ADDRESSEE: BELCHAM & COARD
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA

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; ZIP: 90025
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,058
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: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/228,208

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FILING DATE: 15-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Adriano, Sarah B.
 REGISTRATION NUMBER: 34,470
 OPERATING SYSTEM NUMBER: 201202000001

REFERENCE/DOCKET NUMBER: 30436.30US11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR STATION 5

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Db 81 YSKTGFNC D G K L G N E S V T F Y L Q N L Y V N Q T D I Y F C K I E V M Y P P P Y L D N E K S N G T I I H V K G K 140

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:27:46 ; Search time 37.55 seconds
(without alignments)
511.794 Million cell updates/sec

Title: US-09-383-551B-14
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Gapop 10.0 , Gapext 0.5

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Number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	136	12.6	220	RWHU28	T-cell surface gly
6	124.5	11.6	218	S24413	T-cell surface gly
7	122	11.3	173	I46197	cell surface prote
8	105.5	9.8	218	I43523	T-cell surface gly
9	89.5	8.3	221	S25168	CHT28 protein - ch
10	88	8.2	263	T16329	hypothetical prote
11	85.5	7.9	658	T39495	hypothetical prote
12	84.5	7.9	223	T09536	cytotoxic T-lympho
13	81.5	7.6	129	C25733	T-cell receptor al
14	81.5	7.6	186	S08614	cytotoxic T-lympho
15	80.5	7.5	336	T15727	hypothetical prote
16	78.5	7.3	470	D81353	threonine synthase
17	78	7.2	504	S45644	cytochrome P450 2K
18	77	7.2	676	H96970	endo-arabinase rel
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20	76.5	7.1	2167	S19444	hypothetical prote
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23	75	7.0	1315	T03167	hypothetical prote
24	74	6.9	471	T04911	hypothetical prote
25	74	6.9	988	T03307	hypothetical 109.6
26	74	6.9	1701	T09127	probable erythrocy
27	73.5	6.8	360	T26270	hypothetical prote
28	73.5	6.8	402	S59477	rdsl protein - fis
29	73.5	6.8	892	S57055	probable membrane

30	73	6.8	148	2	JC7235	receptor-activity-
31	73	6.8	972	2	F71608	hypothetical prote
32	72.5	6.7	461	2	S34498	phocostem II chl
33	72.5	6.7	476	2	T27618	hypothetical prote
34	72.5	6.7	492	2	T30066	hypothetical prote
35	72.5	6.7	726	2	JQ2162	A-type inclusion p
36	72	6.7	490	2	T15097	hypothetical prote
37	72	6.7	657	1	F0V2FV	major core protein
38	71.5	6.6	418	2	S42073	aspartic proteinas
39	71.5	6.6	457	2	A54604	regulatory proteina
40	71.5	6.6	576	1	H71414	probable cytochrom
41	71.5	6.6	1256	2	T03096	CDO protein - rat
42	71.5	6.6	2339	1	A42566	omega-conotoxin-se
43	71	6.6	229	1	WMAD51	late 33k protein -
44	71	6.6	585	2	S43718	malate dehydrogena
45	71	6.6	964	2	E71460	probable outer mem

ALIGNMENTS

RESULT 1

JC7397

activation-inducible lymphocyte immuno-mediatory molecule-2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000

C:Accession: JC7397; PC7100

R:Tezuka, K.; Tsujil, T.; Hirano, D.; Tamatani, T.; Sakamaki, K.; Kobayashi, Y.; Kanad

Biochem. Biophys. Res. Commun. 276, 335-345, 2000

A:Title: Identification and characterization of rat AILIM/ICOS, a novel T-cell costim

A:Reference number: JC7396

A:Contents: Spleen

A:Accession: JC7397

A:Molecule type: mRNA

A:Residues: 1-200 <TEZ>

A:Cross-references: DBJ:AB023134

A:Accession: PC7100

A:Molecule type: protein

A:Residues: 21-40 <TE2>

C:Comment: This protein is an inducible cell surface glycoprotein, and a type I trans on, and plays an important role for the maturation or selection of T cells in thymus.

C:Genetics:

A:Gene: ailim-2

C:Keywords: glycoprotein; T-cell; transmembrane protein

Query Match 84.3%; Score 907; DB 2; Length 200;

Best Local Similarity 84.0%; Pred. No. 1.1e-80;

Matches 168; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 MKPYFCHVFVFCFLIRLLTGINGSADHRMFSFHNGVQISCKYPTVQOLKMLFRERE 60

Db 1 MKPYFCHVFVFCFLIRLLTGELNDLNRHMFSDHGVQISCKYPTVQOLKMLFKDRE 60

QY 61 VLCELTGKSGNAVKIPMLCLYHLSNNSVSFFLNPDSSQGSYVFCSLSTFFDPPFPQ 120

Db 61 VLCDLTGKSGNTVSIKIPMLCPYQLSNNSVSFFLDNADSSQGSYVFCSLSTFFDPPFPQ 120

QY 121 ERNLGGYLHIYESQLCCQLKWLPGVLPVGVVLLFGCILIIWFSKKYSSVHPDNPSE 180

Db 121 ERNLGGYLLIYESQLCCQLKWLPGVCAAFVALLFGCIFIWFAKKYRVSVDHPDNPSE 180

QY 181 YMFMAAVNTNKKSLAGVTS 200

Db 181 YMFMAAVNTNKKSLAGMTS 200

RESULT 2

JC7396

activation-inducible lymphocyte immuno-mediatory molecule-1 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000

C:Accession: JC7396; PC7099

R:Tezuka, K.; Tsuji, T.; Hirano, D.; Tamatani, T.; Sakamaki, K.; Kobayashi, Y.; Kamada, Blochem. Biophys. Res. Commun. 276, 335-345, 2000
A:Title: Identification and characterization of rat AILIM/ICOS, a novel T-cell costimulatory molecule
A:Reference number: JC7396
A:Contents: Splenon
A:Accession: JC7396
A:Molecule type: mRNA
A:Residues: 1-216 <TE2>
A:Cross-references: DDBJ:AB023133
A:Accession: PC7099
A:Molecule type: protein
A:Residues: 21-40 <TE2>
A:Comment: This protein is an inducible cell surface glycoprotein, and a type I transmembrane protein, and plays an important role for the maturation or selection of T cells in thymus.
C:Genetics:
A:Gene: ailim-1
C:Keywords: glycoprotein; T-cell; transmembrane protein

Query Match 83.4%; Score 897; DB 2; Length 216;
Best Local Similarity 84.3%; Pred. No. 1,1e-79;
Matches 166; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 1 MKPYCHVVFVFCFLIRLLTGEINGSADHRMFSFHNGGVOISCKYPETVQOLKMLRFRERE 60
Db 1 MKPYCHVVFVFCFLIRLLTGEINGSADHRMFSFHNGGVOISCKYPETVQOLKMLRFRERE 60
QY 61 VLCELTKTGSGNNAVSIKPNMCLVHLNNSVSFFLNPDSSQGSYFCSLSFIFDPPFPQ 120
Db 61 VLCDLTKTGSGNTVSIKPNMCPQLNSNSVSFFLDNADSSQGSYFCSLSFIFDPPFPQ 120
QY 121 ERNLGGYLHIYESQLCCQLKWLPGVLPFAFVVVLLFGCILIIWFSKKYSGSVHDPNSE 180
Db 121 EKNLSGYYLIVESQLCCQLKWLPGCAAFVALLFGCIFIWFAKKYSSVHDPNSE 180
QY 181 YMFMAAVNTNKKSLRAG 197
Db 181 YMFMAAVNTNKKSLRAG 197

RESULT 3
S78540
Inducible T-cell co-stimulator ICOS precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 07-May-1999
C:Accession: S78540; S78748; S78749
R:Kroccek, R.
Submitted to the Protein Sequence Database, June 1998
Reference number: S78540
Accession: S78540
A:Molecule type: mRNA
A:Residues: 1-199 <KRO>
A:Experimental source: cell line MOLT-4V
R:Hutloff, A.; Dittrich, A.M.; Beier, K.C.; Eljaschewitsch, B.; Kraft, R.; Anagnostopoulou, N.; Kroczek, R.; Nature 397, 263-266, 1999
A:Title: ICOS is an inducible T-cell co-stimulator structurally and functionally related to B7-1
A:Reference number: S78748; MUID:99127892
A:Accession: S78748
A:Molecule type: mRNA
A:Residues: 1-199 <HUT1>
A:Experimental source: cell line MOLT-4V
A:Accession: S78749
A:Molecule type: protein
A:Residues: 'X', 193-198 <HUT2>
A:Experimental source: cell line MOLT-4V
C:Complex: homodimer
C:Superfamily: immunoglobulin homology
C:Keywords: dimer; glycoprotein; T-cell; transmembrane protein
F:1-19/Domain: (or 1-20) signal sequence #status predicted <SIG>
F:20-159/Product: (or 21-199) inducible costimulator ICOS #status predicted <MAT>
F:21-138/Domain: extracellular #status predicted <EXT>
F:26-132/Domain: immunoglobulin homology <IMM>
F:139-164/Domain: transmembrane #status predicted <TM>

F:165-199/Domain: intracellular #status predicted <INT>
F:23,89,110/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.1%; Score 722.5; DB 2; Length 199;
Best Local Similarity 68.3%; Pred. No. 9.2e-63;
Matches 136; Conservative 20; Mismatches 42; Indels 1; Gaps 1;

QY 1 MKPYCHVVFVFCFLIRLLTGEINGSADHRMFSFHNGGVOISCKYPETVQOLKMLRFRERE 60
Db 1 MKSGLWYFFLCIRLITLGEINGSANYEMFIFHNGVOILCKYPDIVQOQFKMLKGGQ 60
QY 61 VLCELTKTGSGNNAVSIKPNMCLVHLNNSVSFFLNPDSSQGSYFCSLSFIFDPPFPQ 120
Db 61 ILCDLTKTGSGNTVSIKSLKCHQSLSNNSVSFFLYNLDSHANYFCNLISIFDPPFPK 120
QY 121 ERNLGGYLHIYESQLCCQLKWLPGVLPFAFVVVLLFGCILIIWFSKKYSGSVHDPNSE 180
Db 121 V-TLGGVLIHYESQLCCQLKFWLPTGCAAFVVVVGILGILICWLTKKKYSSVHDNPE 179
QY 181 YMFMAAVNTNKKSLRAGVT 199
Db 180 YMFRAVNTAKSLRDTVT 198

RESULT 4
I46689
CD28 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 21-Jan-2000
C:Accession: I46689
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole
A:Reference number: I46689; MUID:95369849
A:Accession: I46689
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-221 <ISO>
A:Cross-references: GB:D49841; NID:g755094; PID:BAA08641.1; PID:g755095
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
F:34-115/Domain: immunoglobulin homology <IMM>

Query Match 12.8%; Score 138; DB 2; Length 221;
Best Local Similarity 24.8%; Pred. No. 6.5e-06;
Matches 41; Conservative 24; Mismatches 66; Indels 34; Gaps 7;

QY 30 MFSFHNGVQISCKYPETV--QOLKMLRFREREVLCELTKTGSGNAVSIKPN----- 80
Db 29 MLVNNNEVNLCKYTNLFSEFRASLYKGADSAVEVCVNG-----NFSHPHFHSTT 83
QY 81 -MLCLYHLNNSVSFFLNPDSSQGSYFCSLSFIFDPPFPQERNLGG-YLHIYESQLC- 137
Db 84 GPNCDGKLGNETVTYLNLYNQDTYFCKIEVMPYPPYLDNEKSNGTIIHVKEQHFCP 143
QY 138 -----COLKWLPGVLP-----FVVVLLFGCILIIWFSKKK 169
Db 144 AHPSPKSTLFWLVVVGAVLAFYSMLYVALFSC-----WMKSKK 184

RESULT 5
RWHU28
T-cell surface glycoprotein CD28 precursor - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
C:Accession: A39983; A45895
R:Aruffo, A.; Seed, B.
Proc. Natl. Acad. Sci. U.S.A. 84, 8573-8577, 1987
A:Title: Molecular cloning of a CD28 cDNA by a high-efficiency COS cell expression sy
A:Reference number: A39983; MUID:88068631
A:Accession: A39983
A:Molecule type: mRNA

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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:33:26 ; Search time 20.28 Seconds
(without alignments)
381.850 Million cell updates/sec

Title: US-09-383-551B-14

Perfect score: 1076

Sequence: 1 MKPYFCHVFVFCFLIRLLTG.....YMEAAVNTNKKSLAGVTS 200

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Top number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	12.8	221	1 CD28_RABIT	P42069 oryctolagus
2	136	12.6	220	1 CD28_HUMAN	P10747 homo sapien
3	131.5	12.2	218	1 CD28_RAT	P31042 rattus norv
4	130.5	12.1	219	1 CD28_BOVIN	Q28071 bos taurus
5	105.5	9.8	218	1 CD28_MOUSE	P31041 mus musculus
6	89.5	8.3	221	1 CD28_CHICK	P31043 gallus gall
7	84.5	7.9	223	1 CTL4_HUMAN	P16410 homo sapien
8	78	7.2	504	1 CPK1_ONCMY	Q93297 oncorhynch
9	76.5	7.1	223	1 CTL4_RABIT	P42072 oryctolagus
10	76.5	7.1	2167	1 YCS2_YEAST	P25356 saccharomyc
11	75.5	7.0	417	1 CAR4_CANAL	P43093 candida alb
12	75.5	7.0	2210	1 RRPO_LYCYVA	P14240 lymphocytic
13	73.5	6.8	402	1 RDS1_SCHPO	P53693 schizosacch
14	73.5	6.8	892	1 HUL4_YEAST	P40985 saccharomyc
15	73.5	6.8	491	1 CPK3_ONCMY	Q93299 oncorhynch
16	73	6.8	491	1 CPK3_ONCMY	Q93299 oncorhynch
17	72.5	6.7	461	1 PSBC_EUGR	P05700 euglena gra
18	72.5	6.7	726	1 ATL1_CAMP	Q05482 camelpox vi
19	72	6.7	657	1 VP4B_FOPPV	P17355 fowlpox vir
20	71.5	6.6	418	1 CAR6_CANAL	P43095 candida alb
21	71.5	6.6	457	1 GAL8_KLULA	O06433 kluyveromyc
22	71.5	6.6	576	1 C973_ARATH	Q23365 arabidopsis
23	71.5	6.6	863	1 Y184_HUMAN	Q14689 homo sapien
24	71.5	6.6	978	1 PEX6_RAT	P54777 rattus norv
25	71.5	6.6	4829	1 BIR6_HUMAN	Q9nr09 homo sapien
26	71	6.6	228	1 V33P_ADE02	P24939 human adeno
27	71	6.6	229	1 V33P_ADE05	P24940 human adeno
28	71	6.6	510	1 ATPA_BUCAP	O51874 buchnera ap
29	71	6.6	585	1 MAOX_MESCR	P37223 mesembryant
30	71	6.6	964	1 PMPE_CHLTR	O84877 chlamydia t
31	70.5	6.6	135	1 YAB0_METJA	Q58480 methanococc
32	70.5	6.6	329	1 CD86_HUMAN	P42081 homo sapien
33	70.5	6.6	879	1 MANB_CAPHI	Q95327 capra hircu

Query Match 12.8%; Score 138; DB 1; Length 221;

ALIGNMENTS

RESULT 1

CD28_RABIT 1
ID CD28_RABIT STANDARD; PRT; 221 AA.
AC P42069;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-2002 (Rel. 41, Last annotation update)
DE T-cell-specific surface glycoprotein CD28 precursor.
GN CD28
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B/J X CHBB:HM;
RX MEDLINE=95369849; PubMed=7642234;
RA Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
RT costimulatory molecules.";
RL Immunogenetics 42:217-220(1995).
CC -!- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
CC AND B7-2 (B70) (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
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CC -----
CC EMBL; D49841; BAA08641.1; -;
CC InterPro: IPR003600; Ig_like.
CC SMART; SM00410; Ig_like; 1.
CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.
CC SIGNAL 1 19
CC CHAIN 20 221
CC BY SIMILARITY.
CC T-CELL-SPECIFIC SURFACE GLYCOPROTEIN
CD28.
CC DOMAIN 20 150
CC TRANSMEM 151 177
CC DOMAIN 178 221
CC POTENTIAL.
CC CYTOPLASMIC (POTENTIAL).
CC IG-LIKE V-TYPE DOMAIN.
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 38 38
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 72 72
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 93 93
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 106 106
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 130 130
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 221 AA; 25307 MW; 3DF652C9CFC14F13 CRC64;

34 70 6.5 527 1 ABRB_ABRPR Q05077 abrus preca
35 69.5 6.5 223 1 CTL4_MOUSE P09793 mus musculus
36 69.5 6.5 411 1 LMP2_RAT P17046 rattus norv
37 69.5 6.5 529 1 TYRO_HUMAN P14679 homo sapien
38 69 6.4 105 1 RSNB_MOUSE Q99p86 mus musculus
39 69 6.4 276 1 END8_STRCO O86820 streptomyce
40 69 6.4 594 1 MG11_MOUSE O60710 mus musculus
41 69 6.4 637 1 NU5M_STRPU P15552 strongyloce
42 69 6.4 790 1 TOP1_DAUCA P93119 daucus caro
43 68.5 6.4 612 1 GIDA_MYCGE P47619 mycoplasma
44 68 6.3 213 1 RIB7_SULSO P95872 sulfolobus
45 68 6.3 343 1 SLAM_MOUSE Q9qum4 mus musculus

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Best Local Similarity 24.8%; Pred. No. 1.3e-06;
Matches 41; Conservative 24; Mismatches 66; Indels 34; Gaps 7;

QY 30 MFSEHNGGVQISCKYPETV--COQKMLRFREREVLCELTKTGSGNAVSIKNP-----80
DB 29 MLUVANNEVNLCKTYNLFSEFRASLYKGDASAVEVCVVG-----NFSHPHQFHSWT 83
QY 81 -MLCLYHLNNSVSFFLNPDSSQGSYFCSLSIFDPPQFQERNLSGG-YLHIYESQLC- 137
DB 84 GFNCDSKLGNEVTFYLNLYNQTDIYFCKIEVMYPPPYLDNEKSNCTIIVKQHFCEP 143
QY 138 -----CQKMLPVLGFLA-----FVVLLFGCILLIWFSSKK 169
DB 144 AHPSPKSTLFWVLVVGAVLAFYSLNLTVALFSC-----WMKSKK 184

RESULT 2
CD28_HUMAN STANDARD; PRT; 220 AA.
ID CD28_HUMAN P10747;
DE 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T-cell-specific surface glycoprotein CD28 precursor (TP44).
GN CD28.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88068631; PubMed=2825196;
RA Aruffo A., Seed B.;
RT "Molecular cloning of a CD28 cDNA by a high-efficiency COS cell
RT expression system.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8573-8577(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90293482; PubMed=2162892;
RA Lee K.P., Taylor C., Petryniak B., Turka L.A., June C.H.,
RA Thompson C.B.;
RT "The genomic organization of the CD28 gene. Implications for the
RT regulation of CD28 mRNA expression and heterogeneity.";
RL J. Immunol. 145:344-352(1990).
CC -!- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
CC AND B7-2 (B70).
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD28 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd28.htm".
CC
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CC -----
CC EMBL; J02988; AAA60581.1; -.
CC EMBL; M37815; AAA51944.1; -.
CC EMBL; M37812; AAA51944.1; JOINED.
CC EMBL; M37813; AAA51944.1; JOINED.
CC EMBL; M37814; AAA51944.1; JOINED.
CC PIR; A39983; RWU028.
CC HSSP; P16410; 1AH1.
CC MIM; 186760; -.
CC InterPro: IPR003600; Ig-like.
CC SMART; SM00410; IG-like; 1.
CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 18
```

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FT CHAIN 19 220 T-CELL-SPECIFIC SURFACE GLYCOPROTEIN
FT DOMAIN 19 152 CD28.
FT TRANSMEM 153 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 180 220 POTENTIAL.
FT DOMAIN 28 137 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 37 37 IG-LIKE V-TYPE DOMAIN.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 220 AA; 25066 MW; 1D9B6552A5878D0F CRC64;

Query Match 12.6%; Score 136; DB 1; Length 220;
Best Local Similarity 26.1%; Pred. No. 2e-06;
Matches 47; Conservative 26; Mismatches 69; Indels 38; Gaps 6;

QY 30 MFSEHNGGVQISCKYPETVQQLKMLRFREREVLCELTKTGSGNAVSI-----77
DB 28 MLVAYDNAVNLSCKY-----SYNLF-SREFRASL--HKGLDSAVEVCVVGNYSQLQ 77
QY 78 ---KNPMLCLYHLNNSVSFFLNPDSSQGSYFCSLSIFDPPQFQERNLSGGLHIYES 134
DB 78 VYSKTGFNCDSKLGNEVTFYLNLYNQTDIYFCKIEVMYPPPYLDNEKSNCTIIVK 137
QY 135 QLCQCLKMLPVLGFLAFVVLVVGFLGCI-----LIWFSSKKYKSSVHDPNSEYMF 184
DB 138 KHLCSPLFPGPSKPFVWLTVVVGVLACVSLVTVAFIIFWVRSKRLH---SDYMM 194

RESULT 3
CD28_RAT STANDARD; PRT; 218 AA.
ID CD28_RAT
AC P31042;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T-cell-specific surface glycoprotein CD28 precursor.
GN CD28.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DA; TISSUE=Lymphoid;
RX MEDLINE=92104640; PubMed=1309509;
RA Clark G.J., Dallman W.J.;
RT "Identification of a cDNA encoding the rat CD28 homologue.";
RL Immunogenetics 35:54-57(1992).
CC -!- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
CC AND B7-2 (B70).
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
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CC -----
CC EMBL; X55288; CAA39003.1; -.
CC PIR; S38722; S38722.
CC InterPro: IPR003600; Ig-like.
CC SMART; SM00410; IG-like; 1.
CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 19
FT CHAIN 20 218 T-CELL-SPECIFIC SURFACE GLYCOPROTEIN
```


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OM protein - protein search, using sw model

Run on: September 18, 2002, 15:34:36 ; Search time 63.42 Seconds
(without alignments)
545.553 Million cell updates/sec

Title: US-09-383-551B-14
Perfect score: 1076
Sequence: 1 MKPYFCHVFVFCFLIRLLTG.....YMFMAAVNTNKKSLAGVTS 200

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Tc number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1063	98.8	200	11 Q9WVS0	Q9WVS0 mus musculus
2	1055	98.0	200	11 Q9JL17	Q9JL17 mus musculus
3	907	84.3	200	11 Q9JL17	Q9JL17 rattus norv
4	897	83.4	216	11 Q9WVR9	Q9WVR9 rattus norv
5	722.5	67.1	199	4 Q9Y6W8	Q9Y6W8 homo sapien
6	136.5	12.7	219	6 Q97630	Q97630 ovnis aries
7	131	12.0	221	6 Q92757	Q92757 felis silve
8	129	12.0	220	6 Q9BDM8	Q9BDM8 macaca neme
9	128	12.0	221	6 Q9N214	Q9N214 felis silve
10	128	11.9	220	6 Q9BDN5	Q9BDN5 cercocebus
11	128	11.9	220	6 Q9BDM6	Q9BDM6 macaca mula
12	127.5	11.8	221	6 Q9N0N8	Q9N0N8 canis fami
13	125	11.6	221	6 Q9GKP3	Q9GKP3 canis fami
14	124	11.5	221	11 Q9JLV4	Q9JLV4 marmota mon
15	122	11.3	173	6 Q92829	Q92829 canis fami
16	120	11.2	220	6 Q9BDN8	Q9BDN8 papio anubi

17	108	10.0	220	6 Q9BDN2	Q9BDN2 callithrix
18	88	8.2	263	5 Q20288	Q20288 caenorhabdi
19	86	8.0	223	6 Q9BDP1	Q9BDP1 aotus trivi
20	86	8.0	612	10 Q9AUC3	Q9AUC3 lycopersico
21	85.5	7.9	658	3 Q94731	Q94731 schizosacch
22	83	7.7	271	10 Q94L31	Q94L31 lycopersico
23	82.5	7.7	223	4 Q96P43	Q96P43 homo sapien
24	80.5	7.5	223	6 Q9BDC4	Q9BDC4 macaca mula
25	80.5	7.5	223	6 Q9BDN7	Q9BDN7 papio anubi
26	80.5	7.5	303	5 Q94638	Q94638 onchocerca
27	80.5	7.5	336	5 Q18339	Q18339 caenorhabdi
28	80.5	7.5	336	6 Q9GJ73	Q9GJ73 saginus oe
29	79.5	7.4	223	11 Q9JLV3	Q9JLV3 marmota mon
30	79	7.3	301	5 Q94634	Q94634 onchocerca
31	79	7.3	579	10 Q9MAG9	Q9MAG9 arabidopsis
32	79	7.3	719	2 Q9AJB1	Q9AJB1 ruminococcu
33	78.5	7.3	221	6 Q28090	Q28090 bos taurus
34	78.5	7.3	470	16 Q9PPA8	Q9PPA8 campylobact
35	78.5	7.3	779	5 Q9XYS8	Q9XYS8 dictyostell
36	77.5	7.2	535	10 Q9FH36	Q9FH36 arabidopsis
37	77	7.2	323	6 Q9BDM9	Q9BDM9 macaca neme
38	77	7.2	323	6 Q9BDM2	Q9BDM2 cercopithe
39	77	7.2	676	16 Q97LI4	Q97LI4 clostridium
40	76.5	7.1	1312	5 Q9ULF4	Q9ULF4 leishmania
41	76	7.1	341	13 Q9IB06	Q9IB06 spherooides
42	76	7.1	379	10 Q94CH7	Q94CH7 arabidopsis
43	76	7.1	687	10 Q9LQ56	Q9LQ56 arabidopsis
44	75.5	7.0	221	6 Q97631	Q97631 ovnis aries
45	75.5	7.0	2167	3 Q07348	Q07348 saccharomyc

ALIGNMENTS

RESULT 1

Q9WVS0 ID Q9WVS0 PRELIMINARY: PRT; 200 AA.
AC Q9WVS0;
DT 01-NOV-1999 (TREMREL. 12, Created)
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
DE PRECURSOR (CCLP PRECURSOR) (SURFACE PROTEIN).
GN CCLP OR ICOS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Tezuka K., Tamatani T.;
RT "Cell surface molecule mediating cell adhesion and signal
transmission.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/C; TISSUE=SPLEEN;
RA Wu D., Giannoni M.A., Kiesecker C.L., Faas S.J., Mickle A.P.,
Matis L.A., Rother R.P.;
RT "CCLP, A novel molecule that regulates T cell activation.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/C; TISSUE=SPLEEN;
RA Mages H.W., Hutloff A., Heuck C., Buchner K., Himmelbauer H.,
Oliveri F., Krocze R.A.;
RT "Molecular cloning and characterization of murine ICOS and
identification of B7 as ICOS ligand.";
RL Eur. J. Immunol. 30:1040-1047(2000).
DR EMBL; AB023132; BAA82126.1; -;
EMBL; AF257230; AAF70099.1; -;

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DR EMBL; AJ250559; CAB71153.1; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 200 AA; 22690 MW; 9B2278E4CAB1DB47 CRC64;

Query Match
Best Local Similarity 98.8%; Score 1063; DB 11; Length 200;
Matches 198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKPYCHVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQOLKMLFRERE 60
DB 1 MKPYCHVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQOLKMLFRERE 60
QY 61 VLCELTKTGSGNAVSIKPNMCLLYHLSNNSVSFFLNPPDSSQSGSYFCSLSIFDPPPFQ 120
DB 61 VLCELTKTGSGNAVSIKPNMCLLYHLSNNSVSFFLNPPDSSQSGSYFCSLSIFDPPPFQ 120
QY 121 ERNLSSGYLHIYESQLCCOLKWLVPGLPAFVAVVLLFGCILLIWFSSKKYGSVVDHPNSE 180
DB 121 ERNLSSGYLHIYESQLCCOLKWLVPGLPAFVAVVLLFGCILLIWFSSKKYGSVVDHPNSE 180
QY 181 YMFMAAVNTNKKSLAGVTS 200
DB 181 YMFMAAVNTNKKSLAGVTS 200

RESULT 2
QJUL17
ID Q9JUL17 PRELIMINARY; PRT; 200 AA.
AC Q9JUL17;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE CD28-RELATED PROTEIN 1 (INDUCIBLE COSTIMULATORY PROTEIN)
DE (FRAGMENT).
GN ICOS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINAL INTRA-EPITHELIUM;
RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
RA Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tafuri-Bladt A.,
RA Campbell P., Chang D., Chiu L., Dai T., Duncan G., Elliott G.S.,
RA Hui A., McCabe S.M., Scully S., Shaklee C.L., Van G., Mak T.W.,
RA Senaldi G.;
RT "T-cell co-stimulation through B7RP-1 and ICOS.";
RL Nature 0:0-0(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Ola;
RA McAdam A.J., Greenwald R.J., Levin M.A., Chernova T., Malenkovich N.,
RA Ling V., Freeman G.J., Sharpe A.H.;
RT "The inducible costimulatory (ICOS) molecule is critical for CD40-
RT mediated antibody class switching.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216748; AAF45150.1; -.
DR EMBL; AF327185; AAG48732.1; -.
DR EMBL; AF327184; AAG48732.1; JOINED.
FT NON_TER 200
SQ SEQUENCE 200 AA; 22709 MW; 87D97F0DC44ADCA7 CRC64;

Query Match
Best Local Similarity 98.0%; Score 1055; DB 11; Length 200;
Matches 197; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKPYCHVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQOLKMLFRERE 60
DB 1 MKPYCHVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQOLKMLFRERE 60
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DB 1 MKPYCHVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQOLKMLFRERE 60
QY 61 VLCELTKTGSGNAVSIKPNMCLLYHLSNNSVSFFLNPPDSSQSGSYFCSLSIFDPPPFQ 120
DB 61 VLCELTKTGSGNAVSIKPNMCLLYHLSNNSVSFFLNPPDSSQSGSYFCSLSIFDPPPFQ 120
QY 121 ERNLSSGYLHIYESQLCCOLKWLVPGLPAFVAVVLLFGCILLIWFSSKKYGSVVDHPNSE 180
DB 121 ERNLSSGYLHIYESQLCCOLKWLVPGLPAFVAVVLLFGCILLIWFSSKKYGSVVDHPNSE 180
QY 181 YMFMAAVNTNKKSLAGVTS 200
DB 181 YMFMAAVNTNKKSLAGVTS 200

RESULT 3
Q9R1T7
ID Q9R1T7 PRELIMINARY; PRT; 200 AA.
AC Q9R1T7;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
DE PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20462959; PubMed=11006126;
RA Tezuka K., Tsuji T., Hirano D., Tamatani T., Sakamaki K.,
RA Kobayashi Y., Kamada M.;
RT "Identification and characterization of rat AILIM/ICOS, a novel T-cell
RT costimulatory molecule, related to the CD28/CTLA4 family.";
RL Biochem. Biophys. Res. Commun. 276:335-345(2000).
DR EMBL; AB023134; BAA82128.1; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 200 AA; 22529 MW; 0A74C35581F129D4 CRC64;

Query Match
Best Local Similarity 84.3%; Score 907; DB 11; Length 200;
Matches 168; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 MKPYCHVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQOLKMLFRERE 60
DB 1 MKPYCHVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQOLKMLFRERE 60
QY 61 VLCELTKTGSGNAVSIKPNMCLLYHLSNNSVSFFLNPPDSSQSGSYFCSLSIFDPPPFQ 120
DB 61 VLCELTKTGSGNAVSIKPNMCLLYHLSNNSVSFFLNPPDSSQSGSYFCSLSIFDPPPFQ 120
QY 121 ERNLSSGYLHIYESQLCCOLKWLVPGLPAFVAVVLLFGCILLIWFSSKKYGSVVDHPNSE 180
DB 121 ERNLSSGYLHIYESQLCCOLKWLVPGLPAFVAVVLLFGCILLIWFSSKKYGSVVDHPNSE 180
QY 181 YMFMAAVNTNKKSLAGVTS 200
DB 181 YMFMAAVNTNKKSLAGVTS 200

RESULT 4
Q9WVR9
ID Q9WVR9 PRELIMINARY; PRT; 216 AA.
AC Q9WVR9;
DT 01-NOV-1999 (TremBLrel. 12, Created)
DT 01-NOV-1999 (TremBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
DE PRECURSOR.
OS Rattus norvegicus (Rat).
```

RT	"Detailed analysis of human ICOS and its ligand."	
RN	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.	
RL	[4]	
RR	SEQUENCE FROM N.A.	
RC	TISSUE=THYMUS;	
RX	MEDLINE=20243570;	
RA	Aicher A., Hayden-Ledbetter M., Brady W.A., Pezutto A.,	
RA	Magaletti D., Buckwalter S., Ledbetter J.A., Clark E.A.;	
RT	"Characterization of human inducible costimulator ligand	
RT	and function."	
RT	J. Immunol. 164:4689-4696(2000).	
DR	EMBL; AB0231135; BAA82129.1; -;	
DR	EMBL; AJ277832; CAC06612.1; -;	
DR	EMBL; AF218312; AAF1301.1; -;	
KW	Signal.	
FT	SIGNAL	1
FT	SEQUENCE	199 AA; 22624 MW; 214EC741C9BDC9FC CRG64;
SQ	POTENTIAL.	20

Query Match	67.1%	Score	722.5	DB 4	Length	199
Best Local Similarity	68.3%	Pred. No.	1.4e-68			
Matches 136; Conservative	20	Mismatches	42	Indels	1	Gaps
1:						
Y	1	MKPFCYHVFCEFLIRLLTGETINGSADHWMFSFHNGGVOISCKYPETVQOLKRWLFRERE	60			
b	1	MSGLWYFFELCLRIRKIVLGEINGSANYEMFIFHNGGVOILCKYDPDVOQFKMQLLKGQ	50			
Y	61	VIGELTKTKGSGNAVSIKNPMICLHLYSNNVSFFYLFNNPDSQGSYFYFCSLIFDPPPFQ	120			
b	61	ILCDLTKTGSGNTVSIKSLFCHSOLSNNVSFFLYNLDSHANYFYCNLSIFDPPPFK	120			
Y	121	ERNLSGGYLHIYESOLCCOLKWLPLVGLPAFVYVLLFGCILITWFSKKYGSVVDHPNSE	180			
b	121	V-TLTGGLHIYESUCCQLKFWLPGCAAFVVCILGCILICWLTKKKKYSVVHDNPE	179			
Y	181	YMFMAAVNTNKKSRLAGVT	199			
b	180	YMFMRVNTAKKSRLTDVT	198			

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RESULT      6
O97630
ID O97630 PRELIMINARY; PRT; 219 AA.
AC O97630;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE T-CELL SPECIFIC SURFACE GLYCOPROTEIN CD28.
GN CD28.
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
OX
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99309828; Pubmed=10380709;
RA Chaplin P.J., Pietrala L.N., Scheerlinck J.P.;
RT "Cloning and sequence comparison of sheep CD28 and CTLA-4.";
RL Immunogenetics 49:583-584(1999).
DR EMBL: AF092739; AAD04379.1; -.
DR InterPro; IPR003600; Ig_like.
DR SMART; SM00410; Ig_like; 1.
SQ SEQUENCE 219 AA; 25158 MW; D50AD339E5BC2327 CRC64;

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Query Match      12.7%; Score 136.5; DB 6; Length 219;
Best Local Similarity 24.7%; Pred. No. 1.7e-06;
Matches 42; Conservative 30; Mismatches 79; Indels 19; Gaps 7;

y 30 MFSFHGGVQIQISKYPETV--QQLKMRLPREVLCELTKTGK--SGNAVSIKNPMLCLY 85
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
b 28 MLVNVNENYLSCKYTYNLFKEEFASLYKGDASVEVCVANGNHHSHLPLOSTNKFNCTV 87

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[illegible]

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RESULT 10
Q9BDN5 PRELIMINARY; PRT; 220 AA.
AC Q9BDN5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CD28 PROTEIN.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344842; AAK37601.1; -.
DR HSSP; P16410; 1AHL.
DR SMART; SM00410; IG_like; 1.
SQ SEQUENCE 220 AA; 25117 MW; 13BD03F7D937388F CRC64;

Query Match 11.9%; Score 128; DB 6; Length 220;
Best Local Similarity 27.1%; Pred. No. 1.4e-05;
Matches 49; Conservative 20; Mismatches 72; Indels 40; Gaps 9;

QY 30 MFSFHNGVQISCKYPETVQQLKMLRFRREVLCETLTKTSGNAVSI----- 77
Db 28 MLVAYDNVNLSCY-----SYNLF-SREFRASL--HKGLDSAVEVCVYGNYSQQLQ 77

QY 78 ---KNPMLCLYLHLSNNSVSFFLNPPDSOGSYFCSLSIFDPPPPFOERNLSSGGLYHIYE 133
Db 78 VYPKTFGCDGKLGNESTVFYQLNLYVNTDIYFCKIEVWYPPPYLDNEKSNGTIIHVGK 137

QY 134 SQLC-----COLKWLVP---GLPAFVVVLLFGCILLIWFSSKKYKGSVHDNPSEYMF 183
Db 138 KHLCPSPLPFGPSKPPFWLVVGGVLACYSLVTVAFRIFFWMSKR-SRLH---SDYMN 193

QY 184 M 184
Db 194 M 194

Query Match 11.9%; Score 128; DB 6; Length 220;
Best Local Similarity 27.1%; Pred. No. 1.4e-05;
Matches 49; Conservative 20; Mismatches 72; Indels 40; Gaps 9;

QY 30 MFSFHNGVQISCKYPETVQQLKMLRFRREVLCETLTKTSGNAVSI----- 77
Db 28 MLVAYDNVNLSCY-----SYNLF-SREFRASL--HKGLDSAVEVCVYGNYSQQLQ 77

QY 78 ---KNPMLCLYLHLSNNSVSFFLNPPDSOGSYFCSLSIFDPPPPFOERNLSSGGLYHIYE 133
Db 78 VYPKTFGCDGKLGNESTVFYQLNLYVNTDIYFCKIEVWYPPPYLDNEKSNGTIIHVGK 137

QY 134 SQLC-----COLKWLVP---GLPAFVVVLLFGCILLIWFSSKKYKGSVHDNPSEYMF 183
Db 138 KHLCPSPLPFGPSKPPFWLVVGGVLACYSLVTVAFRIFFWMSKR-SRLH---SDYMN 193

QY 184 M 184
Db 194 M 194

Query Match 11.9%; Score 128; DB 6; Length 220;
Best Local Similarity 27.1%; Pred. No. 1.4e-05;
Matches 49; Conservative 20; Mismatches 72; Indels 40; Gaps 9;

QY 30 MFSFHNGVQISCKYPETVQQLKMLRFRREVLCETLTKTSGNAVSI----- 77
Db 28 MLVAYDNVNLSCY-----SYNLF-SREFRASL--HKGLDSAVEVCVYGNYSQQLQ 77

QY 78 ---KNPMLCLYLHLSNNSVSFFLNPPDSOGSYFCSLSIFDPPPPFOERNLSSGGLYHIYE 133
Db 78 VYPKTFGCDGKLGNESTVFYQLNLYVNTDIYFCKIEVWYPPPYLDNEKSNGTIIHVGK 137

QY 134 SQLC-----COLKWLVP---GLPAFVVVLLFGCILLIWFSSKKYKGSVHDNPSEYMF 183
Db 138 KHLCPSPLPFGPSKPPFWLVVGGVLACYSLVTVAFRIFFWMSKR-SRLH---SDYMN 193

QY 184 M 184
Db 194 M 194
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DR SMART; SM00410; IG_like; 1.
KW Signal. 1 18 POTENTIAL.
FT SIGNAL 34 34 N -> S.
FT VARIANT 70 70 E -> G.
FT VARIANT 71 71 D -> N.
FT VARIANT 83 83 E -> G.
FT VARIANT 122 122 Y -> N.
FT VARIANT 175 175 S -> C.
FT VARIANT 209 209 C -> Y.
SQ SEQUENCE 220 AA; 25125 MW; 03776183006AE042 CRC64;

Query Match 11.9%; Score 128; DB 6; Length 220;
Best Local Similarity 25.4%; Pred. No. 1.4e-05;
Matches 46; Conservative 24; Mismatches 71; Indels 40; Gaps 7;

QY 30 MFSFHNGVQISCKYPETVQQLKMLRFRREVLCETLTKTSGNAVSI----- 77
Db 28 MLVAYDNVNLSCY-----SYNLF-SREFRASL--HKGLDSAVEVCVYEDYSQQLQ 77

QY 78 ---KNPMLCLYLHLSNNSVSFFLNPPDSOGSYFCSLSIFDPPPPFOERNLSSGGLYHIYES 134
Db 78 VYSKTEFNCDGKLGNESTVFYQLNLYVNTDIYFCKIEVWYPPPYLDNEKSNGTIIHEKG 137

QY 135 QLCCQLKWLVPGLPAFVVVLLFGCIL-----IIFSKKKYKGSVHDNPSEYMF 183
Db 138 KHLCPSPLPFGPSKPPFWLVVGGVLACYSLVTVAFRIFFWMSKR-SRLH---SDYMN 193

QY 184 M 184
Db 194 M 194

RESULT 12
Q9N0N8 PRELIMINARY; PRT; 221 AA.
AC Q9N0N8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE T-CELL COSTIMULATORY MOLECULE CD28.
GN CD28.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BRED BEAGLE;
RX MEDLINE=21189496; PubMed=11292534;
RA Khatlani T.S., Ma Z., Okuda M., Onishi T.;
RT "Molecular cloning and sequencing of canine T-cell costimulatory
RT molecule (CD28).";
RL Vet. Immunol. Immunopathol. 78:341-348(2001).
DR EMBL; AF259962; AAF72533.1; -.
DR InterPro; IPR003600; Ig_Like.
DR SMART; SM00410; IG_like; 1.
SQ SEQUENCE 221 AA; 25364 MW; 0CCE7EB595EA1E3A CRC64;

Query Match 11.8%; Score 127.5; DB 6; Length 221;
Best Local Similarity 25.4%; Pred. No. 1.6e-05;
Matches 48; Conservative 26; Mismatches 74; Indels 41; Gaps 9;

QY 34 HNGGVQISCKYPETV--QQLKMLRFRREVLCETLTKTSGNAVSIKNPML-----CL 84
Db 33 YNNEVNLSCKYTYNLFSEKFRASLTKGVDSAVEVCVYVNGNYS-----HQQFYSSTGDCD 88

QY 85 YHLSNNSVSFFLNPPDSOGSYFCSLSIFDPPPPFOERNLSSGGLYHIYESQLC----- 137
Db 89 GKLGNETVTFYLRNLRFVNTDIYFCKIEVWYPPPYIGNEKSNGTIIHVKHKLCPDELFP 148
```

QY 138 -COLKWLPLVGLPAFVVVLLFGCILI-----TWFSKKYKGSVHDNPSEYMFMAAVNTN 190
Db 149 DSSKPFWLVVVGAAA---VLVFSYLLVTVALCAYWIKSK-----SSRILOSDYM-----N 194
QY 191 KKSRLAGVT 199
Db 195 MTPREAGPT 203

RESULT 13
Q9GKP3 ID Q9GKP3 PRELIMINARY; PRT; 221 AA.
AC Q9GKP3
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE COSTIMULATORY MOLECULE B7 RECEPTOR CD28.
GN CD28.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang S., Sim G.-K.
RT "Nucleotide and Predicted Amino Acid Sequences of Canine CD28.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF154842; AAG43370.1;
DR InterPro: IPR003600; Ig_like.
DR SMART; SM00410; Ig_like; 1.
KW Receptor.
SQ SEQUENCE 221 AA; 25417 MW; 7BCE7EB595F66AFD CRC64;

Query Match 11.6%; Score 125; DB 6; Length 221;
Best Local Similarity 25.3%; Pred. No. 2.9e-05;
Matches 44; Conservative 26; Mismatches 70; Indels 34; Gaps 8;
QY 34 HNGGVOISCKYPETV--QOLKMLRFRERVLCELTKTGSGNAVSINKPML-----CL 84
Db 33 YNNEVNLSCYYNLFSEKFRASLYKGVDSAVEVCVVGNGYS-----HQPFYSTGDCD 88
QY 85 YHLSNNSVSFFLNPDSSQGSYYFCSLTFDPPQERNLSCG-YLHIYESOLC----- 137
Db 89 GKLGNETVTFYLRNLVFNQTDYFCKIEVMYPPYVIGNEKSNGTIIHVKEKHLCPDELFP 148
QY 138 -COLKWLPLVGLPAFVVVLLFGCILI-----TWFSKKYKGSVHDNPSEYMF 184
Db 149 DSSKPFWLVVVGAAA---VLVFSYLLVTVALCAYWIKSK-----SSRILOSDYMNM 195

RESULT 14
Q9JLV4 ID Q9JLV4 PRELIMINARY; PRT; 221 AA.
AC Q9JLV4
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CD28 ANTIGEN
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RA Lu M., Yang D., Kemper T., Maier A., Roggendorf M.;
RT "Molecular characterization of woodchuck CD28 and cytotoxic T-
lymphocyte associated antigen 4 (CTLA-4).";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF130427; AAF36501.1;
DR InterPro: IPR003600; Ig_like.
DR SMART; SM00410; Ig_like; 1.

SQ SEQUENCE 221 AA; 25594 MW; B29D32E987CE51D1 CRC64;
Query Match 11.5%; Score 124; DB 11; Length 221;
Best Local Similarity 25.8%; Pred. No. 3.7e-05;
Matches 39; Conservative 23; Mismatches 53; Indels 36; Gaps 6;
QY 34 HNGGVOISCKYPETVQOLKMLRFRERVLCELTKTGSGNAVSINKPML----- 82
Db 33 YNNEVNLSCYY-----TYNLF-SKEFRASLYKGVDSAVEVCVVGNGFSHOLQFYSHTG 84
QY 83 --CLYHLSNNSVSFFLNPDSSQGSYYFCSLTFDPPQERNLSCG-YLHIYESOLCQ 139
Db 85 FNCDCGLGNETVTFYLRNLVFNQTDYFCKIEVMYPPYVLDNEKSNGTIVHKENNIC-- 142
QY 140 LKLWLPVGLPA-----FVWLLFGCILI 164
Db 143 -----PGVSPPEPKPFWTLVVFSGVLGIY 167

RESULT 15
Q28289 ID Q28289 PRELIMINARY; PRT; 173 AA.
AC Q28289
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CELL SURFACE PROTEIN (FRAGMENT).
GN CD28.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BEAGLE;
RX MEDLINE=94222451; PubMed=8168859;
RA Pastori R.L., Milde K.F., Alejandro R.;
RT "Molecular cloning of the dog homologue of the lymphocyte antigen
CD28.";
RL Immunogenetics 39:373-373(1994).
DR EMBL; L22178; AAA51453.1;
DR InterPro: IPR003600; Ig_like.
DR SMART; SM00410; Ig_like; 1.
FT NON_TER 1
FT NON_TER 173
SQ SEQUENCE 173 AA; 19770 MW; 7C265AE40931C1EA CRC64;

Query Match 11.3%; Score 122; DB 6; Length 173;
Best Local Similarity 24.8%; Pred. No. 4.5e-05;
Matches 35; Conservative 29; Mismatches 61; Indels 16; Gaps 6;
QY 34 HNGGVOISCKYPETV--QOLKMLRFRERVLCELTKTGSGNAVSINKPML-----CL 84
Db 14 YNNEVNLSCYYNLFSEKFRASLYKGVDSAVEVCVVGNGYS-----HQPFYSTGDCD 69
QY 85 YHLSNNSVSFFLNPDSSQGSYYFCSLTFDPPQERNLSCG-YLHIYESOLCQKLM 143
Db 70 GKLGNETVTFYLRNLVFNQTDYFCKIEVMYPPYVIGNEKSNGTIIHVKEKHLCPD-ELF 128
QY 144 LPVGLPAFVVVLLFGCILI 164
Db 129 -PDSSKPFWLVVVGAVLVFY 148

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Job time: 485 sec

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